

86257

STIC-Biotech/ChemLib

Fr m: Bui, Phuong
Sent: Friday, February 07, 2003 12:00 PM
To: STIC-Biotech/ChemLib
Subj ct: 09/857612 sequence search request

Please search in both commercial and interference databases the following sequences:

- 1) n.a. SEQ ID NO:13
- 2) a.a. SEQ ID NO:14
- 3) DNA encoding SEQ ID NO:14

Thank You. Phuong.

Phuong Bui
305-1996
CM1 Office 9A09, Mailbox 9E12
AU 1638

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: Bob
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 2-20-03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or mary.hale@uspto.gov

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:10:36 ; Search time 2449 seconds
(without alignments)
15828.884 Million cell updates/sec

Title: US-09-857-612a-13
Perfect score: 1332
Sequence: 1 atgaagaagaacagaaga.....gtaattgttttcgsgtaaa 1332

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_in: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rod: *
36: em_htg_mem: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	449.6	33.8	1299	6	AX090309 Sequence
2	449.6	33.8	1299	8	AX133614 Arabidops
3	449.6	33.8	1457	8	AF367326 Arabidops
4	448	33.6	1498	8	AY087433 Arabidops
5	369.4	27.7	833	8	AF209909 Prunus du
6	298.2	22.4	1562	6	AX037586 Sequence
7	298.2	22.4	1562	6	AX037605 Sequence
8	298.2	22.4	99690	8	AC004557 Genomic s
9	249	18.7	264	6	AX090319 Sequence
10	206	15.5	273	6	AX090320 Sequence
11	197.6	14.8	134188	2	AC120983 Oryza sat
12	125	9.4	123620	8	AC103891 Oryza sat
13	122.8	9.2	139534	2	AP005640 Oryza sat
14	121.6	9.1	147348	8	AP004073 Oryza sat
15	96.2	7.2	128210	2	AP005643 Oryza sat
16	91.4	6.9	246	11	AL773076 Arabidops
17	88.2	6.6	1346	10	RN062803 Rattus norv
18	87	6.5	147203	8	AP003687 Oryza sat
19	86.6	6.5	1362	10	RN062803 Rattus norv
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21	79.6	6.0	1354	10	BC028861 Mus muscu
22	76.8	5.8	1155	6	AX090327 Sequence
23	76.6	5.8	1338	4	AF272861 Tupai
24	65.8	4.9	1341	4	RABLCAT
25	65.8	4.9	134374	2	AC121465 Rattus no
26	65.8	4.9	251055	2	AC094385 Rattus no
27	64.6	4.8	1297	9	HUMLCATG
28	64.6	4.8	1355	6	HUMLCATG
29	64.6	4.8	1307	9	HUMLCATG
30	64.6	4.8	1360	9	BC014781 Homo sapi
31	64.6	4.8	1447	9	HSLCAT1
32	64.6	4.8	1744	6	AX077318 Sequence
33	64.6	4.8	1744	6	AX409598 Sequence
34	64.6	4.8	1744	9	HUMLCAT
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36	64	4.8	1137	6	E26768 Novel prote
37	64	4.8	1236	6	E26773 Novel prote
38	64	4.8	1239	10	AF468958 Mus muscu
39	64	4.8	2721	10	BC019373 Mus muscu
40	61.2	4.6	73944	3	AC006402 Drosophil
41	61.2	4.6	182901	3	AC093198 Drosophil
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43	61.2	4.6	309928	3	AE003666 Drosophil
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45	60.4	4.5	1146	6	E26769 Novel prote

ALIGNMENTS

RESULT 1
AX090309 LOCUS 1299 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 2 from Patent WO0116308.
ACCESSION AX090309
VERSION AX090309.1 GI:13444179
KEYWORDS
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS Lasserre M. and van Eenennaam A.
TITLE Plant sterol acyltransferases

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: NO 0116308-A 2 08-MAR-2001;
 MONSANTO COMPANY (US)
 FEATURES Location/Qualifiers
 source 1. 1299
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 BASE COUNT 356 a 289 c 314 g 340 t
 ORIGIN

Query Match 33.8%; Score 449.6; DB 6; Length 1299;
 Best Local Similarity 62.4%; Pred. No. 8.7e-109;
 Matches 786; Conservative 0; Mismatches 444; Indels 30; Gaps 4:

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OY 45 ACTCAGATTACAGTAGTGTGTGTGCTGTGCATGTTGTAACACATGTTGGGAGCA 104
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DB 90 CCTGACCTTTGATTCTTTGTTCCAGGAAACGAGGTAACGAGGTAACGAGGTTGA 149
OY 165 CAATCAGTACAGCCCTTACTTCTGCAATCATGTCACCTTCATCAAGAAAA 224
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OY 225 GA---ATGAGTGGTTACAGCTTTGTTGATTCACAGTGTCTATCTTCTACTCA 281
DB 210 GAGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 269
OY 282 ATGCTTTGGGCAAGCCATACCTTCATTTACACCAAGAACGTCATGATTACTTCAAC 341
DB 270 GTGCTTACAGCCGATCAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 329
OY 342 TCCCTGGGGTGAAGCCGGGCTCTCTACTTGTGTTCCACCAACTCTCTCTATCTCA 401
DB 330 TCCCTGGTGTCAAAACCCGGGTTCTCTATTTGGTTGACCAATCTCTCTATCTCA 389
OY 402 TCCCTGCTCAAGATACCCGATACATGTCACCCCTGTGT---AGATTCTTACAAA 458
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DB 630 AGGAGGCTATTTGCTCTACAACTAATTAAGAAACCCCTTGTGGCCGCAAAAAATT 689
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OY 759 CTTTGCTCTGTGCAACATTTGGGAGTGCCTTATGAGACCTTTATTAAGGAGATGA 818
DB 750 ATTTGCTCTGTGCAACACTGCTGCTGCTTGTGCTTGTGCTTGTGCTGCTGCTGCTG 809
OY 819 ACAAGAAGCTCTGAGAGTAACTTGGCTTTTGGCTTAAACCAAAATTTTT---GCTCC 875
DB 810 TCAGAGGACCTCTCGAGATTAACCAATGGCTACTTCTACCAAGTGTGTGTGTGTGTGT 869
OY 876 TCAGAAACCAATTAAGTATCAATTAAGGCTTATTAAGGCTTATTAAGGCTTATTAAG 935
DB 870 AACTTAACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 929

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OY 936 TCTAAAGACATTTGTTTCTGTAAGGGTTTATCTTATGAAACGAAATCTACCTT 995
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 OY 1116 TGGGATGCTGATGAGACCGTGAACCTTGTGAGCTTTGTGGCCCTTCAATCATGAA 1175
 DB 1110 TGGAGATGAGATGGGACCGTTAATTTGGCAGCTTACGACGCTT----- 1154
 OY 1176 AGAGGAGAAATATCAATTAATGTTAACTGTTAAAGATAGATGGGTCTCATCTTCA 1235
 DB 1155 -----GAAAGTCTGATAGCTTGAACACCGTAGAGATGATGAGTTTCCATATCAT 1208
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 DB 1209 ACTTAAGAGAGATGCTGACATTAAGAGATTTATGAAGAGATTTCAATTAATTAATGA 1268

RESULT 2
 AY133614 1299 bp mRNA linear PLN 07-AUG-2002
 LOCUS Arabidopsis thaliana At1g27480/FL17L21_28 mRNA, complete cds.
 DEFINITION AY133614.1 GI:22137197
 ACCESSION AY133614.1
 VERSION AY133614.1
 KEYWORDS FLI,CDNA.
 SOURCE
 ORGANISM Arabidopsis thaliana
 thale cress.
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 1 (bases 1 to 1299)
 Cheuk, R., Chen, H., Kim, C.J., Shin, P., Banh, J., Bowser, L., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Arabidopsis ORF clones
 Unpublished
 2 (bases 1 to 1299)
 Cheuk, R., Chen, H., Kim, C.J., Shin, P., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

TITLE
 JOURNAL
 COMMENT
 Submitted (17-JUL-2002) Salk Institute Genomic Analysis Laboratory (StGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFI cDNAs (RAFI cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members constructed and sequenced the PUN1 (ORF) clones using the RAFI cDNAs: Cheuk, R., Chen, H., Kim, C.J., Shin, P., Banh, J., Bowser, L., Chan, M.M., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M.,

DEFINITION Arabidopsis thaliana clone 35408 mRNA, complete sequence.
ACCESSION AY087433
VERSION AY087433.1 GI:21406157
KEYWORDS FLI.CDNA.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS 1 (bases 1 to 1498)
Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE Full-length messenger RNA sequences greatly improve genome annotation
JOURNAL Genome Biol. (2002) In press
REFERENCE 2 (bases 1 to 1498)
AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
TITLE Full-length cDNA from Arabidopsis thaliana
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1498)
AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants; including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the WS or Ler ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
FEATURES
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BASE COUNT 425 a 322 c 343 g 408 t
ORIGIN

Query Match 33.68; Score 448; DB 8; Length 1498;
Best Local Similarity 62.33; Pred. No. 2.3e-108;
Matches 785; Conservative 0; Mismatches 445; Indels 30; Gaps 4;
QY 45 ACTACAGTTACAGTAGTGTGTGATGCTGCTCATTTGCTATGACATGTGGCGCAAGAA 104
DB 111 AGTATAGCGGATCTGCTGTGGAGACGATGACTCGATGCTCAAGCTGTGGGTAGCAA 170
QY 105 CCTGACCCCTTTGATTTAATACAGTAACGAGGAAACCACTAGAAAGCAAGTTGAC 164
DB 171 TGTGTACCCCTTTGATTTGCTGTCCAGAAACGAGGATTAACGAGTAGAGTAGGGCTGA 230
QY 165 CAATCAGTACAAAGCCCTTACTTTATCTGCGAATCATAGTGATCCCTCATCAAAAAA 224
DB 221 CAGAGAAATACAAAGCCAGTAGTGCTGTAGTAGCAGCTGTGTATATCCGATTCATAGAA 290
QY 225 GA--ATGATNGTTCAGACTTGTGTTGATTCAGTGCATACACTTGCCTTACCTA 281
DB 291 GAGTGTGATAGTGTTAGGCTATGTTGATGATCAGACAGTGTATTTGTCTTACACAG 350
QY 282 ATGCTTTCGCCAAGCATGACCTTCATTATACCCCAAGAACTCATGATTTACTTCAAC 341
DB 351 GTCCTTACAGCATGCAATGATGTGTATGATACCCCTGATTTGGATGATACCAATGTC 410
QY 342 TCTGTGGGTGAGACCGGGTCCCTCACTTTGTTGTTCCACCAACTCTTCTATCTCAA 401
DB 411 TCTGTGTTCCAAACCCGGGTCTCATTTGGTTCCAGCAATCATCTTATACCTCGA 470
QY 402 TCCCTGCTCAAGCATATACCGGATATGATGACGACCCCTGGT--AGATTCATTA 458
DB 471 CCTGTCTCCGAGATGCTCCACATCTTACATGAGACATTTGGTGAAGCTTAGAGAA 530
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DB 591 GGTGCTTCGGGCCACCCGCTCCGTAGCCACAGTTCACAAAGCACTTCAAAATTT 650
QY 579 GATAGAAAGCAACCAATTCATTAATGGAAGCAGATGATCTTCCACAGATT 638
DB 651 GGTGAAAGAACTTACAGCAGAGAAAGAAAGCAAGATGATCTCTCCATAGCT 710
QY 639 AGGAGGCTATTTGTCTCTACAACTAATAATGAACCCCTTGTGGCGCAAAATTT 698
DB 711 AGGAGACTTTTGTCTCTACAACTAATAATGAACCCCTTGTGGCGCGCAAGTA 770
QY 699 CATCAACACTTATGCTCTTTCAGCTCATGGGTTGTGTATAGAGAAATTAAC 758
DB 771 CATCAACACTTGTGTGACCTGCGCGCATGGGTTGTGATCTCATATCAATCAAC 830
QY 759 CTTTCATCTGGCAGCACTTTGGAGTGGCCCTATGAGCCCTTATTAAGAGGATGA 818
DB 831 ATTGCTTCTGACACACACTGGGTGCTCTTATTAACCTTTGCTGTAGACGGCA 890
QY 819 ACAAGAAAGCTCGAGAGTAACCTTTGGCTTTGCTTAACCCCAAAATTTT--GCTCC 875
DB 891 TCAGAGACCTCGAGAGTAACCAATGCTACTTCCATCTACCAAGGTTCACAGACG 950
QY 876 TCAAAACCAATAGTATACCTCCAAATTAAGCTTATTCAGCTATGACATGATGATTT 935
DB 951 AACTTAACCGCTTGTGTAACCTCCAGAGTTTAACATACAGCTTACGATGATGATG 1010
QY 936 TCTAAACACATGTTTCTTCCGAGGAGTTATTCCTATGAACAACTTACCTCC 995
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QY 996 GATAGGAAATTAAGAACCAAGAGTCCCTATACCTGTATTAAGGAGAGGAGTGG 1055
DB 1071 AACGAGAGCTGATGACTCCGGAGTGCACACTTGTCATATATGGAGAGAGTGA 1130
QY 1056 AACCTTGAACATTTGTTTATGGAAGAGTGATTTGATGAGGCGCAAGAAATTCATA 1115
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QY 1116 TGGGATGCTATGGAAGGGAAGTGTGATGATGATGATGATGATGATGATGATG 1175
DB 1191 TGGAGATGAGATGAGAGGCTTAATTTGGCAGCTTACAGCTTT----- 1235
QY 1176 AGAGGAGAAATCAATACCTTAAGTGTGATTAAGATGAGGAGTGTCTATCTCAAT 1235
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Result 5	AF209909	833 bp	DNA	Linear	PLN_03-JAN-2000
LOCUS	AF209909				
DEFINITION	Prunus dulcis lecithin-cholesterol acyl transferase (LCAT1) gene,				
ACCESSION	AF209909				
VERSION	AF209909.1				
KEYWORDS	GI:6653737				
SOURCE	Prunus dulcis.				
ORGANISM	Prunus dulcis				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.				
AUTHORS	1 (bases 1 to 833)				
TITLE	Ma,R.C. and Oliveira,M.M.				
JOURNAL	Molecular Cloning of A Lecithin-Cholesterol Acyl Transferase Homolog Gene from Almond (Prunus dulcis)				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 833)				
TITLE	Ma,R.C. and Oliveira,M.M.				
JOURNAL	Direct Submission				
FEATURES	Submitted (01-DEC-1999) Lab of Plant Genetic Engineering, Instituto de Biologia Experimental e Tecnologica, Quinta do Marquês, Oeiras/Lisboa, Lisboa Apct.12-2/80, Portugal				
SOURCE	Location/Qualifiers				
gene	1..833				
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[illegible]

[illegible]

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OY	560	TCGAAGATCTAAGAATTTTGATAGAAGACGACCAATTCATATATGGAAGCCAGTGA	619
Db	89305	TACAGACCTCCAAACAAATTTGGTGAAGAAAACACTAGCAGCGAGAACGAAAGCAAGTGA	89364
OY	620	TACCTCTCTCCACAGTTTAGAGGCCATATTTGTCCTCAACTACTAATATGAACCCCC	679
Db	89365	TACTCTCTCCCAATGACCTAGAGAGACCTTTTGTCTCTCAATTTCTCAACCGTACACCC	89424
OY	680	CCCTTTGGCGCAAAAATTCATCAACACCTTCATTCCTTTACGCTCCATGGGGTGGTG	739
Db	89425	CTTCATGGCGCCCGCAAGTATCATCAACACTTTTGTTCACCTGCTCCTGCGCATGGGTGGGA	89484
OY	740	CTATGAGCAAAATGTATACACTTTTGCATCTGGCAACACTTTGGAGTGGCCCTAGTGACC	799
Db	89485	CGATCTCTCAGATGAAGACATTTTGCTTGGCAACACACTCGGTGTCTCTTAGTTAAC	89544
OY	800	CTTTATTTAGTGAAGGATATACAAAGAACCTCCGAGAGTAACTTTTGGCTTTTGCTTAACC	859
Db	89545	CTTTCCTGGTGCAGAGCGGATCAGAGACCTCCGAAAGTAAACCAATGGCTACTTCCATCTA	89604
OY	860	CAAAAATTTTGGTCTCTCAA---AAACCAATATGATATACCTCCATTTAGGCTTAATTCG	916
Db	89605	CCAAAGTGTTCACGACAGAACTAAACCGCTTGTCTGTAACCTCCAGSTTAATCAACAG	89664
OY	917	CTCATGACATGCTGTTATTTTCTAAAGACATTTGTTTCTGAAAGGGSTTTATCCTATG	976
Db	89665	CTTACGAGATGATGATGGGTTTTTTGCAGACATTTGGATTTCTCAACAAAGATTTGCTTACA	89724
OY	977	AAACACGAATTCACCTCTTGATAGGGAACATPAAAGCACACCAAGTGCCTATTAACCTTGA	1036
Db	89725	AGACAAAGATGTGGCTTTTAAACAGAGAGAGCTGATACCTCGGAGTGGCCACTGACTTGA	89784
OY	1037	TTATGGGAACGGAGATGGGAACCTTGGAAACATTTGTTTATGGAAGAGTATTTTGATG	1096
Db	89785	TATATGGAGAGAGATTTATACCCGAGGTTTGTATATATGGAAGAAAGAGATTCGATG	89844
OY	1097	AACGCCACGAATATCATATGAGGATGGATGATGAGAACGCTGAACCTTGGTGAAGCTTGTGG	1156
Db	89845	AGCAACAGAGATTTAAGTATGAGATGAGATGGAGATGGACGTTAATTTGGCGAGCTTAGCAG	89904
OY	1157	CGCTTCAATCACTATGAGAAAGAGAAAAATCAATACCTTAAAGTGTTAAGATAGATG	1216
Db	89905	CTTT-----GAAAGTCGATAGCTTGAACACCGTAGAGATTTGATG	89943
OY	1217	GGGTCTCTCATCTCATCTACTTAAAGATGGAAGTTGCACCTAAATGAATATAGAGTGAGA	1276
Db	89944	GAGTTTGCATACATCTTACTTAAAGACGAGATGCGACTTAAAGATTTATGAAGCAGA	90003
OY	1277	TTACTTCAATTAATTTCTCA 1295	
Db	90004	TTTCAATTATTTATTTATGCA 90022	
RESULT 9			
LOCUS	AX090319	264 bp	DNA
DEFINITION	Sequence 12 from Patent WO0116308.	Linear	PAT 21-MAR-2001
ACCESSION	AX090319		
VERSION	AX090319.1	GI:13444185	
KEYWORDS			
SOURCE	soybean.		
ORGANISM	Glycine max		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.		
AUTHORS	1 (bases 1 to 264)		
TITLE	Lassner M. and van Benneham A.		
JOURNAL	Plant sterol acyltransferases Patent: WO 0116308-A 12-08-MAR-2001; MONSANTO COMPANY (US)		

FEATURES Location/Qualifiers
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 /organism="Glycine max"
 /db_xref="taxon:3847"
 unsure 39
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 /note="n=unknown"
 BASE COUNT 62 a 73 c 52 g 74 t 3 others
 ORIGIN

Query Match 18.7%; Score 249; DB 6; Length 264;
 Best Local Similarity 98.5%; Pred. No. 2.7e-55;
 Matches 260; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 315 CCAGAGACGAGTACTTCAACACCTCGGTGGGTGAGACCGGTCCTCATTGG 374
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 DB 1 CCAGAGACTCGAGTACTTCAACACCTCGGTGGGTGAGACCGGTCCTCATTGG 60

OY 375 TTCACCAACTCTCTTCT-ATCTCAATCTCTGCTCAAGCATATCACCGATACATGG 433
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 DB 61 TTCACCAACTCTCTTCTCTCATCTCAATCTCTGCTCAAGCATATCACCGATACATGG 120

OY 434 CACCCCTGGTAGATTCAATTAACAAGCTTGCTACGCTGATGTAGACTCTGTTTGAG 493
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 DB 121 CACCCCTGGTAGATTCAATTAACAAGCTTGCTACGCTGATGTAGACTCTGTTTGAG 180

OY 494 CCCCTTAGCTTTAGATATGCTAGCTGCTGAAGGTACCCCTTACAAAGTGGTTCCA 553
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 DB 181 CCCCTTAGCTTTAGATATGCTAGCTGCTGAAGGTACCCCTTACAAAGTGGTTCCA 240

OY 554 AGTTCCTCAAGATCTAAAGAATT 577
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 DB 241 NGTTCCTCAAGATCTAAAGAATT 264

RESULT 10
 LOCUS AX090320 273 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 13 from Patent WO0116308.
 ACCESSION AX090320
 VERSION AX090320.1 GI:13444186
 KEYWORDS
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1 (bases 1 to 273)
 AUTHORS Lässner, M. and van Eenennaam, A.
 TITLE Plant sterol acyltransferases
 JOURNAL Patent: WO 0116308-A 13 08-MAR-2001;
 MONSANTO COMPANY (US)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:3847"
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 252
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 265..266
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 272
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 BASE COUNT 80 a 56 c 62 g 69 t 6 others
 ORIGIN

Query Match 15.5%; Score 206; DB 6; Length 273;
 Best Local Similarity 97.7%; Pred. No. 7.6e-44;
 Matches 217; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 1 ATGAGAGAGCAAGCAAGAGGCTGCAAGATTGAGGTTGTACACTACATACAGTA 60
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 DB 53 ATGAGAGAGCAAGCAAGAGGCTGCAAGATTGAGGTTGTACACTACATACAGTA 112

OY 61 GTTGTGTGATGCTGTCATTGTATGCATGTGGGGCAAGCAACCTGACCTTTGATT 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 113 GTTGTGTGATGCTGTCATTGTATGCATGTGGGGCAAGCAACCTGACCTTTGATT 172

OY 121 CTAATACAGGTAACGAGGAGCAACACTAGACAGAGTTACCAATACATACAGGCC 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 173 CTAATACAGGTAACGAGGAGCAACACTAGACAGAGTTACCAATACATACAGGCC 232

OY 181 TCTACTTCATCTCGGAATCATGATACCTCTCATCAGAGAA 222
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 233 TCTACTTCATCTCGG-ATCNTGTATCCTCTCANNAAGANA 273

RESULT 11
 LOCUS AC120983/C 134188 bp DNA linear HTG 21-JUN-2002
 DEFINITION Oryza sativa chromosome 3 clone OSJNB0011H13, *** SEQUENCING IN
 PROGRESS ***, 4 ordered pieces.
 ACCESSION AC120983
 VERSION AC120983.1 GI:20564440
 KEYWORDS HTG; HTGS; PHASE2.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 134188)
 AUTHORS Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Tallon, L., Gansberger, K.,
 Kim, M., Overton, II, U., Bera, D., Tsilini, T., Krol, M., Jarrahl, B.,
 Jin, S., Koo, R., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.,
 Utecherbach, T., Feldblyum, T., Yang, Q., Haas, B., Suh, B., Peterson, J.,
 Quackenbush, J., White, O., Salzberg, S. and Fraser, C.
 Oryza sativa ssp. japonica cv. Nipponbare OSJNB0011H13 BAC genomic
 sequence
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 134188)
 AUTHORS Buell, R.
 TITLE Direct Submission
 JOURNAL Submitted (14-MAY-2002) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 COMMENT * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 61218: contig of 61218 bp in length
 * 61219 61256: gap of unknown length
 * 61257 77652: contig of 16396 bp in length
 * 77653 77727: gap of unknown length
 * 77728 131160: contig of 53433 bp in length
 * 131161 131197: gap of unknown length
 * 131198 134188: contig of 2991 bp in length.
 FEATURES Location/Qualifiers
 source 1..134188
 /organism="Oryza sativa"
 /cultivar="Nipponbare"
 /db_xref="taxon:4530"
 /chromosome="3"
 /clone="OSJNB0011H13"
 /note="japonica cultivar-group"
 BASE COUNT 39144 a 28013 c 28230 g 38642 t 159 others

ORIGIN

Query Match	14.8%;	Score 197.6;	DB 2;	Length 134188;
Best Local Similarity	50.9%;	Pred. No. 9.7e-42;		
Matches 650;	Conservative	0;	Mismatches 534;	Indels 92; Gaps 4;

OY	104	ACACGACCCCTTTGTTATTTATTAACAGGTAACGGGAGGAACCAACTATAGAACAGCTTGA	163
Db	77046	AGCTGCACCCGGGTGATCTGTATCCCGGCGCGGGGGGAAACCAAGTGGAGGGCGGGCTGA	76987
OY	164	CCAATCACTAACGAAGCCCTCTACTTTCATCTCATCTCGAATCATGTATACCTCTCATCAAGAAAA	223
Db	76986	CGAGGAGATAGCCGCCCGCTGAGACCTCGGGTGGCGGGCTGG --- CCGGTGGTGGCGGGC	76930
OY	224	AGAAATGATGGTTTCAGACTTTGGTTTGATTCACAGTGTATACTTGCTCTTCACTCAAT	283
Db	76929	GGCGGGGTGGTTCGGCTCTGTGTTTCGACCCGCTCGTGTGTGGCGCGGCTACCAAGGT	76870
OY	284	GCTTTGGCGAAGCGATGACCCCTTCAATTATCCACCAAGAACTGGATGATTAATCTCAACACTC	343
Db	76869	GCTTCGCCGACCGGATGACCTCTTTCTAGCATTCGCTGCCGAGCATACGCAAGCTC	76810
OY	344	CTGGGGTTGAGACCGCGGGTCCCTCACTTTGGTTCCACCACACTCTCTTCTATCTCAATC	403
Db	76809	CCGGGTGAGACCAACGAGGTCTCCGACTTCGGGTCCACTCCACCTCCGCTACCTCGAC	76750
OY	404	CTCGTCTCAACATTA-----	418
Db	76749	CCAACCTCAAGTACGATTTCTACTATCAGCAATTCACGCGTTGTGTTGGTGTAT	76690
OY	419	-----TCACCGGATCATGGACCCCT	440
Db	76689	GACCGGATTCGAATTTGCAATTTGGATGTGTAGTTGCTTAACGGGTGATCATGACGTGTT	76630
OY	441	GGTAGATTCATTACAAAAGCTTGGCTACGCTGATGGTGAAGACTGTGTTTGAAGCCCTTA	500
Db	76629	GGCGAGCACGCTGGAGAGGACGAGGTGAGAGAAAGGTTTCGACCTGTTCCGGCGCCGTA	76570
OY	501	TGACTTTTGATATGTGTCTAGCTGCTGAAGGTACCCCTTACAAAGTGGGTTCCAACTTCT	560
Db	76569	CGACTTCCGGTACGGGGCTGGCGGGGCCGGGACACCCGCTGGGTGTGGCAGAGCGCTACT	76510
OY	561	CAAAAGATTTAAAGAAATTTGATAGAAAGCAAGCAACATTCATAATTTGGGAAGCCAGTAT	620
Db	76509	GGAGCGCGCTGAGAAAGCTGTGTGAAGTCCGCGCTGGCGGCCCAACGGCGGGAGCGCCGAT	76450
OY	621	ACTTCTCTCCACAGATTATAGAGGCGCTATTGTCTCTACACTACTAATAATAGAAACCCCC	680
Db	76449	CTCTGTGGCGCAACCGCTGGCGGGCGCTGACGCGCTGCAGATGGTGGCGGAGGCCCCC	76390
OY	681	CTCTTGGCGCAAAAAATTCATCAAAACACTTCATTCCTTTTACGTCCATGGGTGTGTGC	740
Db	76389	CGCGTGGCGCCCGCGAAGCTGAACCGGCTGGTGCAGTGTCCCGGCGCTGGGGGGGGTTC	76330
OY	741	TATAGACCAAAATGTACACTTTGCTATCTGGCAACACTTTGGAGAGCCCTTAGTGGACCC	800
Db	76329	GGTGAAGAGATNGCTACACTTCGCGTGGCGGCAACACCTCGCGCTGTGCTGTGAGGC	76270
OY	801	TTTATTTAGTGAAGGATGACAAGAAAGCTCCGAGAGTAACTTTGGCTTTTGCCTAACCC	860
Db	76269	GTCGCTCATCCGCGACGAGCGACCGCACCGCGAGAGCAACTGTGTGGCTGTCCGGCGCC	76210
OY	861	AAAAATTTTGGTCTCAAAAACCAATAGT---GATAACTCCAATTAGCGCTTATTCAGC	917
Db	76209	GGGGTGTTCGGGAACACCAACGCTGTGTGTGCGGGCAACCAACCGGTCTTACTCCGC	76150
OY	918	TCATGACATGTTGATTTTCTAAAAGCAATTTGTTTCTGAAAGGGGTTTATCTCTATGA	977
Db	76149	CAAGAACATGACGAGCTTCTCCGGGACATCGGGTTTCCGAAAGGGGTGGAGCCGTACCG	76090
OY	978	AACACGAATTTACCTCTGATATGGGACACATATAAGCACACAGATGCTTATTACTTTGAT	1037
Db	76089	GGAGGGATATAGCGCGCTGTCTGTGAGGTCTCCCGGAGCCGGGGTGGCGGTGATCTGCT	76030

QY	1038	TATGGAAACGGAGTGGGAACTTGGAAACATTGTTTATATGGAAAGGATTTGTGATA	1097
Db	76029	CGTGGCAACGGGCGCTGCACACCGTGAGAGCTCGGTACGGGAGAGGGGCTTGAGGC	75970
QY	1098	ACGGCCACAGAA---TATCATATGGGATGGTATGGAACGGTGAACCTTGAGCTTGT	1154
Db	75969	CGGGCCGGAGGAGGTGTGTACGGGACGGGACGGGAGCGTCAACCTGCAGACCTGCT	75910
QY	1155	GGCGCTTCATCTATGGAAGAAGAGAGAAAAATCAATACCTTAAAGTGGTAAAGATAGA	1214
Db	75909	CGGGCCGATCAAGGCGTGGTCCGACTCGCGGAGAGAGGTGTGGAGGTGTGACCTGCC	75850
QY	1215	TGGGCTGTCTCACTTCACTTCAATCTTAAGGATGAATTCGACTCAATTAAGTATAGTAGTGA	1274
Db	75849	CGAGGTGTGCGACCTCCGGGATCTCTCAAGSACAAGAAGCGGCGCTCGAACAGATCTTGAGGAT	75790
QY	1275	GATTACTTCATTAAT	1290
Db	75789	CATGACGCCATCAAT	75774

	AC103891	AC103891	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORANISM
RESULT 12									
AC103891									
LOCUS	AC103891	123620 bp	DNA						
DEFINITION	Oryza sativa (japonica cultivar-group)		linear						
	Oj1175C11, complete sequence.			chromosome 3	clone				
ACCESSION	AC103891								
VERSION	AC103891.2	GI:20279375							
KEYWORDS	HTG.								
SOURCE	Oryza sativa (japonica cultivar-group).								
ORANISM	Oryza sativa (japonica cultivar-group)								

REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; Ehrhartoideae: Oryzae; Oryza.
AUTHORS	1 (bases 1 to 123620)
TITLE	Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Sasaki,C., Henry,D., Oates,R. and Simmons,J.
JOURNAL	Rice Genomic Sequence
REFERENCE	2 (bases 1 to 123620)
AUTHORS	Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Sasaki,C., Henry,D., Oates,R. and Simmons,J.
TITLE	Direct Submission
JOURNAL	Submitted (30-NOV-2001) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
REFERENCE	3 (bases 1 to 123620)
AUTHORS	Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Sasaki,C., Henry,D., Oates,R. and Simmons,J.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
REFERENCE	4 (bases 1 to 123620)
AUTHORS	Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H., Rambo,T., Sasaki,C., Henry,D., Oates,R., Simmons,J., Thurmond,S.K. and Sun,S.
TITLE	Direct Submission
JOURNAL	Submitted (26-APR-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
COMMENT	On Apr 24, 2002 this sequence version replaced g1:17155018. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. Bacterial transposons can be found throughout the project at these locations: 120370-123043, 96027-98926, 96146-98910, 94511-97689, 64299-66589 and 11325-14898. From base 43413-43417 there is only a single subclone. There are 2 bases below standard at 96468-69. At base 93692 there is either a G or a pad - Clemson University reads disagree with Monsanto data here. The nucleotide sequence of this BAC clone was generated by combining Monsanto and Clemson University Genomics Institute


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          /gene="O01175C11.9"
          /note="contains similarity to RING zinc finger protein"
CDS       complement(101n(34294..34456,34580..34704,34769..35317
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20178..22247
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RLGSLAVMKCYSDNLSREKREERPSGAVALQWVGCDVSGDEGRSMVACRDEEV
GIGGVDVRRKATAPAVACDSATAAHTGRGVRGVMOWSARSHDGLPWLAORRDA
YARHAPWRRRORPOKGNPKDLIRACIRLLTGTNGSCISISHRNTYHPLTIRP
EPGLERLRINNSYTEYGRIPRYGSHSGSPEDDSHTIPAAEGASTSKAPYLEDSIR
LRRRLARLCMGWSEKRVOLGAEEGDVAIVDRMRPMDIOATVAAHISARGVGAVERD
GRGLIAYGANDPBGHRTTTTDARAANKSKISCELDFTIVILLICLSNAIKYIRCYPSD
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GNSMRLLTMACRKNLKIARKIMPARRRGIDLPAPATARRRRIODAGGPP
LIPSTSVVVEVAASPPTPANRSRIEAEELSLPPPPRCRRGGCTERRAANGDSE
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Best Local Similarity 49.5%; Pred. No. 1.7e-21;
Matches 372; Conservative 0; Mismatches 374; Indels 6; Gaps 2;
Oy 416 ATATACCGGATACATGACACCCCTGTAGATTCAATTACAAAGCTTGACGCTGATG 475
Db 134826 ATAGGAGCGTGTGCATGGAGAGGCTCTGTGAGGCCCTGGAAAGAGAGGATACGGCGAGG 134885
Oy 476 GTGAGACTCTGTTTGGACCCCTTATGACTTATGATATGATGCTGTACCTGTGAGTCAAC 535
Db 134886 GAGAACACTGTGTGGCGCCCGCGTACGACTTACAGTACGCGCGCCCTCCCGCTTGC 134945
Oy 536 CTTACAGTGGGTTCCAAAGTTCTCAAAAGATCTAAGAATTTGATAGAACGACGA 595
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Oy 596 ATTCAATAATAGGAGGACGATGATCTTCTCCACAGTTTATAGAGGCGATTTGTC 655
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Oy 656 TACAACTACTAAATGAACACCCCTCTTGCGCGCAAAATTCATCAACACTTCATTTG 715
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Db 135126 TGCTCTGCTCGGCGCTGCGGCGCTGCGGTGACATGTGGCCCTCGCTCTGCA 135185
Oy 776 CTTTGGAGTGCCTTATGACACCTTTATTAAGTAGGAGTGAACAAAGAGCTCCGAGA 835
Db 135186 TCCTCTGCTGCTGCTGTGTTGGGAGACGCTGCTAGCTAGCGGAACAGGACTTCGCA 135245
Oy 836 GTAACTTTGGCTTGGCTTGAACCCCAAAATTTTGGTCTCTCAAAACCAATAGTATAA 895
Db 135246 GCATGTTCTCTCTCTGCTGCGCGTGGCGGGGTGTACGG---CGACACGCCACTGGTATCA 135302
Oy 896 CTCGAATTAGGCTTATTCAGCTCATGACATGCTTATTTCTAAGAACATTTGTTTC 955
Db 135303 CGCGAGCCAAAGACTACCTCGCGCGACATGCGGAGTTTCTCTCGCGGCTGGTTTCT 135362
Oy 956 C---TGAAGGGTTTATTCCTTATGAACACGAATTCACCTGTATAGGAACATTAANG 1012
Db 135363 CGAGCAGAGGTGGCGCTTACCGCGGAGGCGCTCCGCTCGCTGATTTCCGGG 135422
Oy 1013 CACCAAGTGCCTTAACTTGTATTTAGGAACGAGAGTGGAGCACTTGAACCATTTGT 1072
Db 135423 CGCCCTCTGCTGCGCTGACGTCATCAACAGGCGTGTGGTGTGCGGCGGTATAGTGTGG 135482
Oy 1073 TTTATGGAAGAGTGTATTTGATGAACGCGCAAGAAATATCATATGAGGATGCTATGAA 1132
Db 135483 TGTCTTGGAGCGGCAACTTTCAGCGCGAAGCCTCAGTGTGTGAACGCGAGCGCATGTGGC 135542
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:08:52 : Search time 224 Seconds
(without alignments)
13391.347 Million cell updates/sec

Title: US-09-857-612a-13
Perfect score: 1332
Sequence: 1 atgaagaagaacaaga.....gtaattgttcggggttaa 1332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No	Score	Query Match Length DB ID	Description
1	1332	100.0	1332 21 AAA49206 Soybean putative 1
2	1148	86.2	1217 21 AAA49202 Soybean putative 1
3	449.6	33.8	1299 22 AAS01081 Arabidopsis thaliana
4	449.6	33.8	1495 21 AAC47273 Arabidopsis thaliana
5	448	33.6	1498 21 AAC39845 Arabidopsis thaliana
6	298.2	22.4	1562 21 AAC64437 Arabidopsis thaliana
7	298.2	22.4	1562 21 AAC64447 Arabidopsis thaliana
8	249	18.7	264 22 AAS01087 Soybean sterol acyl
9	208	15.6	1500 21 AAA49204 Corn putative lec1

10	206	15.5	273	22	AAS01088	Soybean sterol acy
11	144	10.8	563	21	AAA69662	Pinus radiata lec1
12	127	9.5	353	21	AAA69561	Pinus radiata lec1
13	105	7.9	542	21	AAA49200	Corn putative lec1
14	95.4	7.2	1660	21	AAA49205	Corn putative lec1
15	86.4	6.5	921	21	AAA49201	Corn putative lec1
16	86	6.5	1440	21	AAA49203	Corn putative lec1
17	76.8	5.8	1155	22	AAS01095	Corn sterol acyltr
18	64.6	4.8	1323	24	ABK87900	CDNA encoding huma
19	64.6	4.8	1358	8	AAAT70191	DNA clone p12 enc
20	64.6	4.8	1744	20	AA232180	Human lecithin cho
21	64.6	4.8	1744	22	AAD02648	Human lecithin-cho
22	64.6	4.8	1744	24	ABN95747	Gene #2245 used to
23	64.6	4.8	1744	24	ABK35510	Human endometrial
24	64.6	4.8	4308	24	AAD02649	DN305 plasmid for
25	64	4.8	1137	19	AAV68563	Murine lecithin-cho
26	64	4.8	1236	19	AAV68568	Murine kidney lec1
27	61.2	4.6	4024	23	ABL21222	Drosophila melanog
28	60.4	4.5	1137	19	AAV68561	Human heart lecith
29	60.4	4.5	1146	19	AAV68564	Human heart lecith
30	60.4	4.5	1236	19	AAV68566	Human heart lecith
31	60.4	4.5	2680	20	AA234023	Human heart lecith
32	60.4	4.5	2680	21	AAC78492	Human PRO540 nucle
33	60.4	4.5	2680	21	AAA68516	Human PRO540 CDNA
34	60.4	4.5	2680	22	AAC31556	Human PRO540 CDNA
35	60.4	4.5	2680	24	ABK69667	CDNA encoding huma
36	60.4	4.5	2681	24	AAH14618	Human cDNA sequenc
37	60.4	4.5	2720	22	AAK94279	Human full-length
38	56.8	4.3	1824	23	ABL21223	Drosophila melanog
39	51.2	3.8	1233	19	AAV68562	Human kidney lecith
40	51.2	3.8	1242	19	AAV68565	Human kidney lecith
41	51.2	3.8	1332	19	AAV68567	Human kidney lecith
42	51.2	3.8	2687	21	AAA26392	Human secreted pro
43	47.8	3.6	1941	23	AA591800	DNA encoding novel
44	47.8	3.6	5700	24	ABK87899	Human lecithin-cho
45	47.8	3.6	6901	18	AAAT78853	Human lecithin-cho

ALIGNMENTS

RESULT 1	
AAA49206	AAA49206 standard; CDNA: 1332 BP.
ID	AAA49206
AC	AAA49206:
XX	12-DEC-2000 (first entry)
XX	Soybean putative lecithin:cholesterol acyltransferase gene #2.
XX	Soybean; lecithin:cholesterol acyltransferase; phytosterol;
KW	phosphatidylcholine-sterol O-acetyltransferase; heat shock; cold shock; ss.
KW	Glycine max.
XX	OS
XX	Key
FT	Location/Qualifiers
FT	1..1332
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FT	/product= "lecithin:cholesterol acyltransferase"
FT	/EC_number= "2.3.1.43"
XX	W0200032791-A2.
XX	08-JUN-2000.
PD	02-DEC-1999; 99WO-us28586.
XX	03-DEC-1998; 98US-0110782.
XX	(DUP0) DU PONT DE NEMOURS & CO E I.
PA	Cahoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;
XX	
PI	

XX	WP1: 2000-412337/35.
DR	P-PStDB: AAB01211.
XX	
PT	Polynucleotide encoding plant lecithin:cholesterol acyltransferase
PT	enzyme useful for producing transgenic plants and for producing
PT	antibodies specific to which is useful for screening cDNA expression
PT	libraries
XX	
PS	Claim 2; Page 46; 49pp; English.
CC	
CC	The present sequence is a putative coding sequence for a soybean
CC	lecithin:cholesterol acyltransferase (also known as
CC	phosphatidylholine:sterol O-acyltransferase) and Apolipoprotein AI and -D.
CC	associated with high-density lipoproteins and Apolipoprotein AI and -D.
CC	The gene and protein can be used to produce transgenic plants which have
CC	increased lipid metabolism and membrane fluidity, and therefore increased
CC	resistance to heat and/or cold shock, to alter the content of phytoesterol
CC	or lecithin in grains and to identify potential herbicides.
CC	
XX	
SQ	Sequence 1332 BP: 385 A; 282 C; 289 G; 376 T; 0 other:
	Query Match 100.0%; Score 1332; DB 21; Length 1332;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ATGAAGAGAACAAGAGGGCTCAAGATTGAGGTGTACACTCAGTTCACAGTA 60
Dd	1 ATGAAGAAGAAACAAGAGGGCTCAAGATTGAGGTGTACACTCAGTTCACAGTA 60
OY	61 GTTGTTGATGCGTGCATNTGCTATGSCAANTGTGGGCGAAGCAACCCTGACCTTTGATT 120
Dd	61 GTTGTTGATGCGTGCATNTGCTATGSCAANTGTGGGCGAAGCAACCCTGACCTTTGATT 120
OY	121 CTAAATACCAAGGTAAACGAGAGGAAACCACTAGAACGAAGTTGACCAATCATGACAAGCCC 180
Dd	121 CTAAATACCAAGGTAAACGAGAGGAAACCACTAGAACGAAGTTGACCAATCATGACAAGCCC 180
OY	181 TCTACTTTCATCTCGCAATCATGTGATGCCCTCTCATCAAGAAAAAGATGGATGTTCCAGA 240
Dd	181 TCTACTTTCATCTCGCAATCATGTGATGCCCTCTCATCAAGAAAAAGATGGATGTTCCAGA 240
OY	241 CTTTGGTTGATTCGACGTCTATTAATTGCTGCTCTTCACTCAATGCTTTGGCCAGACGATG 300
Dd	241 CTTTGGTTGATTCGACGTCTATTAATTGCTGCTCTTCACTCAATGCTTTGGCCAGACGATG 300
OY	301 ACCGTCATTTACCAACCAAGAACTGATATTAATCTTCAACACATCGTGGGGTTGAGACCCGG 360
Dd	301 ACCGTCATTTACCAACCAAGAACTGATATTAATCTTCAACACATCGTGGGGTTGAGACCCGG 360
OY	361 GTCCCTCACTTGTGTCCACCAACATCTGTCTCTATTCATCAATCCGTCACAGATATTC 420
Dd	361 GTCCCTCACTTGTGTCCACCAACATCTGTCTCTATTCATCAATCCGTCACAGATATTC 420
OY	421 ACCGGATATCATGGCACCCCTGGTAGATTTCATTAACAAAAGCTTGGCTACGCTGATGGTAG 480
Dd	421 ACCGGATATCATGGCACCCCTGGTAGATTTCATTAACAAAAGCTTGGCTACGCTGATGGTAG 480
OY	481 ACTCTGTTTGGAGGCCCTTATAGACTTTCAGATATGATGCTAGCTGCTGAAAGGTACACCTTCA 540
Dd	481 ACTCTGTTTGGAGGCCCTTATAGACTTTCAGATATGATGCTAGCTGCTGAAAGGTACACCTTCA 540
OY	541 CAAGTGGTTTCAAGTTCCTCAAAGATTTAAAGAAATTTGATAGAAAGCAAGCAAAATTC 600
Dd	541 CAAGTGGTTTCAAGTTCCTCAAAGATTTAAAGAAATTTGATAGAAAGCAAGCAAAATTC 600
OY	601 AATAATGGGAAGCCAGTATATCTCTCTCCACACATTTAGAGAGGCTATTGTCCTACAA 660
Dd	601 AATAATGGGAAGCCAGTATATCTCTCTCCACACATTTAGAGAGGCTATTGTCCTACAA 660
OY	661 CTACTAATAATAGAAACCCCTCTTTGGGCGAAAAAATTCATCAACACTTCATGCTCTT 720
Dd	661 CTACTAATAATAGAAACCCCTCTTTGGGCGAAAAAATTCATCAACACTTCATGCTCTT 720

Accession	Gene	Species	Position (nt)	Sequence	Length (nt)
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Db 721	TCACCTCCATGGGGTGGTGGCTATATAGACGAAATGTACACCTTGGCATCTGGCAACACTTGG	Soybean	12-DEC-2000	TCACCTCCATGGGGTGGTGGCTATATAGACGAAATGTACACCTTGGCATCTGGCAACACTTGG	780
QY 781	GGAGTGGCCCTAGTGAACCTTTATTAGTAGGAGGATGAACCAAGAAAGCTCCGAGAGTAAC	Soybean	12-DEC-2000	GGAGTGGCCCTAGTGAACCTTTATTAGTAGGAGGATGAACCAAGAAAGCTCCGAGAGTAAC	840
Db 781	GGAGTGGCCCTAGTGAACCTTTATTAGTAGGAGGATGAACCAAGAAAGCTCCGAGAGTAAC	Soybean	12-DEC-2000	GGAGTGGCCCTAGTGAACCTTTATTAGTAGGAGGATGAACCAAGAAAGCTCCGAGAGTAAC	840
QY 841	CTTTGGCTTTTGGCTAACCCAAAATTTTTTGGTCCTCAAAACCAATAGTGTAACTCCA	Soybean	12-DEC-2000	CTTTGGCTTTTGGCTAACCCAAAATTTTTTGGTCCTCAAAACCAATAGTGTAACTCCA	900
Db 841	CTTTGGCTTTTGGCTAACCCAAAATTTTTTGGTCCTCAAAACCAATAGTGTAACTCCA	Soybean	12-DEC-2000	CTTTGGCTTTTGGCTAACCCAAAATTTTTTGGTCCTCAAAACCAATAGTGTAACTCCA	900
QY 901	ATTAGGCGCTTATTCAGGTCATGACATGATGGTTGATTTCTCTAAAGACATTTGTTCTGAA	Soybean	12-DEC-2000	ATTAGGCGCTTATTCAGGTCATGACATGATGGTTGATTTCTCTAAAGACATTTGTTCTGAA	960
Db 901	ATTAGGCGCTTATTCAGGTCATGACATGATGGTTGATTTCTCTAAAGACATTTGTTCTGAA	Soybean	12-DEC-2000	ATTAGGCGCTTATTCAGGTCATGACATGATGGTTGATTTCTCTAAAGACATTTGTTCTGAA	960
QY 961	GGGGTTTATCCTTATGAACACGCAATTTCTACCTTGATAGGAGACATMAAAGCACACAA	Soybean	12-DEC-2000	GGGGTTTATCCTTATGAACACGCAATTTCTACCTTGATAGGAGACATMAAAGCACACAA	1020
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Db 1261	GAATTAAGTATGATGGGGGTGTCTCACTCAATCAATGAAGATGAAGTTCGACTAAT	Soybean	12-DEC-2000	GAATTAAGTATGATGGGGGTGTCTCACTCAATCAATGAAGATGAAGTTCGACTAAT	1320
QY 1321	TTTTTGGGGGTAA 1332	Soybean	12-DEC-2000	TTTTTGGGGGTAA 1332	1332
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RESULT 2	AAAA9202 standard; cDNA; 1217 BP.	Soybean	12-DEC-2000	AAAA9202 standard; cDNA; 1217 BP.	1217
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XX	Soybean putative lecithin:cholesterol acyltransferase gene #1.	Soybean	12-DEC-2000	Soybean putative lecithin:cholesterol acyltransferase gene #1.	1217
XX	Soybean; lecithin:cholesterol acyltransferase; phytosterol;	Soybean	12-DEC-2000	Soybean; lecithin:cholesterol acyltransferase; phytosterol;	1217
KM	phosphatidylcholine-sterol O-acetyltransferase; heat shock; cold shock; ss.	Soybean	12-DEC-2000	phosphatidylcholine-sterol O-acetyltransferase; heat shock; cold shock; ss.	1217
XX	Glycine max.	Soybean	12-DEC-2000	Glycine max.	1217
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XX 03-DEC-1998; 98US-0110782.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E.I.
XX
XX Cahoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;
XX WPI: 2000-412337/35.
XX P-PsDB; AAB01207.
XX
XX Polynucleotide encoding plant lecithin:cholesterol acyltransferase
XX enzyme useful for producing transgenic plants and for producing
XX antibodies specific to which is useful for screening cDNA expression
XX libraries
XX
XX Claim 2; Page 38; 49pp; English.
XX
XX The present sequence is a putative coding sequence for a soybean
XX lecithin:cholesterol acyltransferase (also known as
XX phosphatidylcholine-sterol O-acyltransferase). This enzyme is found
XX associated with high-density lipoproteins and Apolipoprotein-AI and -D.
XX The gene and protein can be used to produce transgenic plants which have
XX increased lipid metabolism and membrane fluidity, and therefore increased
XX resistance to heat and/or cold shock, to alter the content of phytosterol
XX or lecithin in grains and to identify potential herbicides.
XX
XX Sequence 1217 BP; 346 A; 250 C; 262 G; 359 T; 0 other:
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XX Query Match 86.2%; Score 1148; DB 21; Length 1217;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 185 CTTTCATCTCGGAATCATAGTACCTCTCATCAGAGAAAAAGATGATGGTTCCAGACTTT 244
DB 1 CTTTCATCTCGGAATCATAGTACCTCTCATCAGAGAAAAAGATGATGGTTCCAGACTTT 60
QY 245 GATTGATTCAGTGTCTACTTGTCTCTCATCATCATGCTTTGCCAGCATGACCC 304
DB 61 GATTGATTCAGTGTCTACTTGTCTCTCTTCACTCATGCTTTGCCAGCATGACCC 120
QY 305 TTTCATACCAACCAAGACTGATGATTACTTCAACACTCTGGGGTTGAGACCCGGGTC 364
DB 121 TTTCATACCAACCAAGACTGATGATTACTTCAACACTCTGGGGTTGAGACCCGGGTC 180
QY 365 CTCACCTTGGTTCACCAACTCTCTCTCTATCTCAATCCCTGCTCAAGCATATACCG 424
DB 181 CTCACCTTGGTTCACCAACTCTCTCTCTATCTCAATCCCTGCTCAAGCATATACCG 240
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QY 485 TGTTTGAGAGCCCTTATGACTTATGATATGCTAGCTGTAAGAGTCAACCTTCACAAG 544
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QY 605 ATGGAGACCAAGTATGATCTCTCCACAGTTTGAAGGCGCTATTTGCCACAACTAC 664
DB 421 ATGGAGACCAAGTATGATCTCTCTCCACAGTTTGAAGGCGCTATTTGCCACAACTAC 480
QY 665 TAAATAGAAACCCCTCTTGGGCAAAAAATTCATCAAAACACTTTCCTTTTTCAG 724
DB 481 TAAATAGAAACCCCTCTTGGGCAAAAAATTCATCAAAACACTTTCCTTTTTCAG 540
QY 725 CTCATGGGGTGTGCTATAGACGAAATGTACACTTTCATCTGGCAACACTTTGGGAG 784
DB 541 CTCATGGGGTGTGCTATAGACGAAATGTACACTTTCATCTGGCAACACTTTGGGAG 600
QY 785 TGCCCTAGTGGACCTTATATTAGAGGATGAACAAGAGTCCGAGACTATTCCTT 844

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DB 601 TGCCCTAGTGGACCTTATATTAGAGGATGAACAAGAGTCCGAGAGTAACCTTT 660
QY 845 GGCCTTTGGCTTAACCCCAAAAATTTTGGTCTCTCAAAAACCAATGATGATCTCCAAFTA 904
DB 661 GGCCTTTGGCTTAACCCCAAAAATTTTGGTCTCTCAAAAACCAATGATGATCTCCAAFTA 720
QY 905 GGCCTTATTCAGCTCATGACATGATGGTTGATTTCTTAAAGACATGTTTCTCTGAAGGG 964
DB 721 GGCCTTATTCAGCTCATGACATGATGGTTGATTTCTTAAAGACATGTTTCTCTGAAGGG 780
QY 965 TTTATCCCTTAAGAAACAGCAATTTCTACCTTGATAGGAGACATTAAGACACACAGTGC 1024
DB 781 TTTATCCCTTAAGAAACAGCAATTTCTACCTTGATAGGAGACATTAAGACACACAGTGC 840
QY 1025 CTATTAACCTTGTATTAATGGAACCGGAGTGGACACCTTGGAAACATTTGTTATGGGAAG 1084
DB 841 CTATTAACCTTGTATTAATGGAACCGGAGTGGAGACCTTGGAAACATTTGTTATGGGAAG 900
QY 1085 GTGATTTTGAAGACGGCCAGAAATATCATATGGGAGTGTGATGGAACGGTGAACCTTG 1144
DB 901 GTGATTTTGAAGACGGCCAGAAATATCATATGGGAGTGTGATGGAACGGTGAACCTTG 960
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QY 1205 TTAAGATTAATGAGGGGTGTCTCATCTTCAATCTTAAGATGAAGTTCACATAAGTAA 1264
DB 1021 TTAAGATTAATGAGGGGTGTCTCATCTTCAATCTTAAGATGAAGTTCACATAAGTAA 1080
QY 1265 TAGTAGTGAGATTAATCTCAATTAATCTCATGCTGAGCTGGTTAGTAAATTTGTTT 1324
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DB 1141 CGGGGTAA 1148

RESULT 3
AAS01081
ID AAS01081 standard; DNA; 1299 BP.
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XX AAS01081;
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XX 31-MAY-2001 (first entry)
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XX Arabidopsis thaliana sterol acyltransferase LCAT1 DNA.
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XX Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
XX acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
XX nutritional supplement; dairy product; food product; salad dressing; ds.
XX
XX Arabidopsis thaliana.
XX
XX OS
XX FH key Location/Qualifiers
XX FT CDS 1..1299
XX FT /*tag= a
XX FT /product= "LCAT1"
XX
XX WO200116308-A2.
XX
XX PD 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US23863.
XX
XX PF 30-AUG-1999; 99US-0152493.
XX
XX PR (MONS ) MONSANTO CO.
XX
XX PA
XX PI Lassner M, Van Eenennaam A;
XX

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DR WPI: 2001-166010/17.
DR P-PsDB: AAU00458.
XX
PT New isolated nucleic acid encoding plant lecithin:cholesterol
PT acyltransferase-like or acyl (coenzyme A) CoA:cholesterol
PT acyltransferase-like polypeptides, for modifying the sterol content and
PT oil production of plants -
XX
XX Claim 5, Page 75; 127p; English

QY	45	ACTCAGACTTTCAGAGTAGTGTGTATCTGTATCTGTCATTTGGCATATGCACATGAGGGGACCA	104
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QY	105	CCTGCAGCCCTTTGATTCTTAATACAGGTACGAGGAGGAACCAACTAGAAACAAAGTTGAC	164
Db	90	CGTGAACCCCTTTGATTCGTGTCTCCAGGAAACGAGAGGTAAACAGCTTAGAGGTACGGCTGGA	149
QY	165	CAATCAGTACAAAGCCCTCTACTTTCATCTGGGAAATCATAGTATACCCCTCATCAAGAAAAA	224
Db	150	CAGAGATATCAAGACCAAGTACTGTCTGTGTAGCAGCTGGTTATATCCGATTCATATAGAA	209
QY	225	GA--ATGATGGTTCAGACTTTGGTTTGATTCCAGTGTCACTACTTGGTCCCTTCACTCA	281
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QY	282	ATGCTTTCCGGAAGCATAGACCCCTTCATTACCAACCAAGCCGATGATTAATTCAACAC	341
Db	270	GTGCTTACGCAATGATGATGTGTACTATAGACCTGATTTGGATGATATCCAAAATGTC	329
QY	342	TCCATGGGGTTGAGACCCGGGTCCCTCACTTTGGTTCACCAACTCTCTCTATCTGAA	401
Db	330	TCCATGGTCCAAAACCCGGGTCTCATTTGGGTTCGACCAAAATCATCTTATACCTGGA	389
QY	402	TCCATGCTCAAGCATATCACCGGATATATGGCACCCCTGGT--AGATTCAATTCAAAA	458
Db	390	CCCTGCTCCAGATGCGACATCTTAATATGGAACATTTTGGAAAGCTTAGAGAAAAA	449
QY	459	GCTTGGCTACGCTATGTTGAGACTCTTTTGGAGCCCTTATGACTTATAGTATGCT	518
Db	450	ATGGGGGATATGTAACGACCAAAACCATCTAGAGACTCCATATGATTTTCAGTAGGGCT	509
QY	519	AGCTGCTGAAGTCAACCTTACAAAGTGGGTTCCAGTTTCTCTCAAGAATCTTAAGCAATTT	578
Db	510	GCGCTGTTCGGGCCACCGTCCGCTGTAGCCCTCACAGTCTCTACAAAGCACTCAAAACAATTT	569

QY	579	GATAGAGAAGCAAGCAATTCCAAATTAATGGGAAGCCAGTATACCTCTCTCCACAGTTT	638
DB	570	GGTGGAAAAAATCAGACCGCAGAGAAAGGAAMCCAGATACCTCTCTCCATAGCCT	629
QY	639	AGGAGCCTATTTGTGCTCACAACACTACTAATAGAAACCCCCCTCTTGGCGCAAAAATT	698
DB	630	AGGAGGACTTTTGCTCTCCCAATTTCTCCAAACCGTACACCCCTTCATATGGCGCGCAAGTA	689
QY	699	CATCAACACATTCATAGTGCWTTCAGCTCCATGGGCGGTGCTATAGACAAATGTACAC	758
DB	690	CATCAACACATTTGTTGTGACCTCGCTCGCCCATGGGTGGGACGATCTCTCAGATGAAGAC	749
QY	759	CTTTGCATCTGGCAACACTTTTGGGAGTGCCCTAGTGGACCCCTTATTAATGAGGATGA	818
DB	750	ATTTCTCTTCGGCAACACACTCGGTGTCCTTTAGTTAACCTTTGTGTGACAGGCA	809
QY	819	ACAAAGAAGCTCCGAGAGTAACCTTTGGCTTTTGCTTAACCCAAAATTTT---GGTCC	875
DB	810	TCAGAGGACCTCCGAGAGTAAACCAATGGCTACTCTCCATCCCAAAAGTGTTCACGACAG	869
QY	876	TCAAAACCAATAGAGTAATCTCCAAATTAGCCCTATTCAGCTCANTGACATGGTTGATTT	935
DB	870	AACCTAACCCGCTTGTCGGTAATCTCCAGTTTAACTACACAGCTTTACGAGATGGATCGTT	929
QY	936	TCTAAAGACATTTGGTTTTCCTGAAGGGGTTTATCCTTATGAACAACGAAATTTACCTT	995
DB	930	TTTTGGACACATTTGGATTTCTCACAAGAGATTTGGCTTTACACACAGAGTGTGGCTTT	989
QY	996	GATAGGAACATTAAGAAGCACCACAGTGCCCTATTACTTTGATTATGGGAAGGGAGTGGG	1055
DB	990	AACAGAGAGCTGTATGATCTCCGGGAGTGCCAGTCACTTCGATTTATGGGAGAGGATTTGA	1044
QY	1056	AACCTTGGAAACATTTGTTTATATGGGAAGTGATTTTATGAAAGCCGCCAGAAATATACATA	1111
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QY	1116	TGGGATGTATGATGAGACCGGTAACCTGTGAGACTTGTGGCCCTTCATCACTATGAAA	1175
DB	1110	TGGAGATGAGATGGAGACGGTAAATTTTGGCGAGCTTAGACAGCTTT-----	1155
QY	1176	AGAGGAGAAAATCAATACCTTTAAAGTGTTAAGATAGATGGGCTGTCCATACCTTCAAT	1233
DB	1155	-----GAAATCGATAGCTTGAACACCGTAGAGATTAATGATGAGGATTTGCGATACATCAT	1200
QY	1236	ACTTAAGATGAAGTGCCTACTAATGAATAGATAGAGTGAATACTTCAATTAATTTCTCA	1295
DB	1209	ACTTAAGACAGATGCCACTTTAAAGATTAATGAAGCAAGATTTCAATTAATTAATATATA	1266

RESULT 4

ID AAC47273 standard; DNA; 1495 BP.

AC AAC47273;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53208.

KW Hybridisation assay; genetic mapping; gene expression control;

KW metabolic pathway; promoter; termination sequence; ss

05 *Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125768.
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XX (BADI) BASF PLANT SCI GMBH.
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XX Dohlqvist A, Stahl U, Lemman M, Banas A, Ronne H, Stymne S;
XX WPI: 2000-665012/64.
XX
XX Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT pathway for triacylglycerol production and DNAs encoding them, useful
PT for producing triacylglycerol, or for transforming any cell or organism
PT to increase oil content -
XX
XX Claim 6; Page 59; 97pp; English.
XX
XX The present invention describes an enzyme for catalysing (in an
CC acyl-CoA-independent reaction) the transfer of fatty acids from
CC phospholipids to diacylglycerol in the biosynthetic pathway for the
CC production of triacylglycerol (TAG). The enzyme is designated as
CC phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and
CC the nucleotides encoding them are useful for producing TAG and/or
CC TAG with uncommon fatty acids. The enzyme and the nucleotide are
CC also useful for transforming any cell or organism in order to be
CC expressed in this cell or organism and result in an altered, preferably
CC increased oil content of this cell or organism. The present sequence
CC represents the Arabidopsis thaliana PDAT genomic DNA.
XX
SQ Sequence 1562 BP; 441 A; 312 C; 367 G; 442 T; 0 other;

Query Match 22.4%; Score 298.2; DB 21; Length 1562;
Best Local Similarity 61.4%; Pred. No. 2,4e-78;
Matches 527; Conservative 0; Mismatches 308; Indels 24; Gaps 2;

QY 440 TGGTAGATTCATTACAAAGCTTGGCTACGCTGATGAGACCTCTGTTGAGACCCCTT 499
DB 694 TGAAGGCTTAGAGAAATAATCGGGTATGTAAACGACCAACATCTTGAAGCTTCAT 753
QY 500 ATGACTTAGATATGCTCTACTGCTGAGTCAACCTTCAAGTGGGTTCCAAAGTTCC 559
DB 754 ATGATTTAGAGTACGGCTGGCTCTCTCGGCGCACCGCTCCCGTTAGCCCTCAAGTTCC 813
QY 560 TCAAGATCTTAAGATTTGATAGAGAAGCAATTCATTAATGGAAGCCAGTGA 619
DB 814 TACAAGACCTCAAAACAAATTTGGTGAAAACTAGCAGCAAGAAAGAAAGCAGAGA 873
QY 620 TACTTCTCCCAACAGTTTAGAGGCTATTTGCTACACACTCTAATTAAGAAACCCC 679
DB 874 TACTCTCTCCATAGGCTTAGAGGACTTTTCTGCTCTCAATTTCTCAACCGTACCAACC 933
QY 680 CCTCTTGGCGCAAAATAATATCAACACTTCATTTGCTTTCAGTCCATGGGGTGGTG 739
DB 934 CTTCATGCGCCCGCAAGTACATCAACACTTTGTCACCTCGTCCGCTAGGGGTGGGA 993
QY 740 CTATAGACGAATGTACACCTTTGCATCTGGCAACACTTTGGGAGTCCCTTAGTGACC 799
DB 994 CGATCTCTCAGATGAAAGACATTTCTCTTGCGCAACACTCGGTGCCCTTTAGTTAAC 1053
QY 800 CTTTATTAGAGGAGATGACAAAGAACGCTCCGAGATTAACCTTTGGCTTTGGCTAAC 859
DB 1054 CTTTGTGCTGACAGCGCATGAGAGACTTCGAGAGTAAACCAATGCTTACTTCCATCTA 1113
QY 860 CAAAATTTTGTGCTCA--AAACCAATAGATGATACCTCAATTAAGGCTTATTCAG 916
DB 1114 CCAAGGTTTCAAGAGAACTAAACCGCTGTCTGTAACCTCCGAGTTTACCTACACAG 1173
QY 917 CTATGATGATGTTGATTTCTTAAGACATGTTTCTCTGTAAGGGGTTTATCTTATG 976
DB 1174 CTACAGATGATGATGTTTCTTGTGACATTTGATTTCTACAGAGGATGTTGCTTACA 1233
QY 977 AAACAGCAATTTCTACCTTATAGGAAACATTAAGACACCAACGATCCCTTAATCTGTA 1036
DB 1234 AGACAAGAGTGTGCTTTTAAACAGAGGATGATGACTCGGGAGTGTCCCACTACCTGCA 1293
QY 1037 TTATGGAGAGGAGTGGAACTTGGAAACATTTTATGAGGAAAGTATTTGATG 1096

DB 1294 TATATGGAGAGAGGATTCATACCGGAGGTTTGTATGTATGAAAAAGAGATTCGATA 1353
QY 1097 AACGGCCAGAAATATCATATGTTGGATGTGATGAGACGGTGAACCTTGTGCTTGGTG 1156
DB 1354 AGCAACCAAGATTAAGATGATGAGATGGACGCTTAATTTGGCGAGCTTAGCAG 1413
QY 1157 CGCTTCATCTACTATGGAAGAGGAAATAATCAATACCTTAAGGTGTTAAGATAGATG 1216
DB 1414 CTTT-----GAAAGTCGATAGCTTTAAGACCCCTAAGATTTGATG 1452
QY 1217 GGGTGTCTCATCTCAATCTTAAAGATGAGTGAAGTTGCAATTAATGATAGGTGAGA 1276
DB 1453 GAGTTTCCCATACATCTTACTTAAAGCAGATCGCACTTAAGAGATTAATGAAAGCAGA 1512
QY 1277 TTACTTCAATTAATTCGA 1295
DB 1513 TTTCAATTAATTAATTAATGA 1531

RESULT 7
AAC64447
ID AAC64447 standard; DNA; 1562 BP.
XX AAC64447:
AC
DT 12-FEB-2001 (first entry)
XX
XX Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:9b.
DE
XX PDAT: phospholipid:diacylglycerol acyltransferase; triacylglycerol;
KW TAG; EST: expressed sequence tag; fatty acid; oil content; ds.
XX
XX Arabidopsis thaliana.
OS
PN W0200060095-A2.
XX
PD 12-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-EP02701.
XX
PR 01-APR-1999; 99EP-0106656.
PR 10-JUN-1999; 99EP-0111321.
PR 07-FEB-2000; 2000US-0180687.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Dohlqvist A, Stahl U, Lemman M, Banas A, Ronne H, Stymne S;
XX WPI: 2000-665012/64.
DR
XX
XX Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT pathway for triacylglycerol production and DNAs encoding them, useful
PT for producing triacylglycerol, or for transforming any cell or organism
PT to increase oil content -
XX
XX Claim 6; Page 93-94; 97pp; English.
XX
XX The present invention describes an enzyme for catalysing (in an
CC acyl-CoA-independent reaction) the transfer of fatty acids from
CC phospholipids to diacylglycerol in the biosynthetic pathway for the
CC production of triacylglycerol (TAG). The enzyme is designated as
CC phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and
CC the nucleotides encoding them are useful for producing TAG and/or
CC TAG with uncommon fatty acids. The enzyme and the nucleotide are
CC also useful for transforming any cell or organism in order to be
CC expressed in this cell or organism and result in an altered, preferably
CC increased oil content of this cell or organism. The present sequence
CC represents the Arabidopsis thaliana PDAT genomic DNA.
XX
SQ Sequence 1562 BP; 441 A; 312 C; 367 G; 442 T; 0 other;

Query Match 22.4%; Score 298.2; DB 21; Length 1562;

Best Local Similarity 61.4%: Pred. No. 2.4e-78;
Matches 527; Conservative 0; Mismatches 308; Indels 24; Gaps 2;

```

OY 440 TGGTGATTCATTACAAAGCTTGCGTACGTCGATGAGACTGCTGTTGGAGCCCTT 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 694 TGAAGCTCTAGAGAAAAATGCGGTATGTTACGACCAACCACTCTTAGAGCTCCAT 753
OY 500 ATGACTTTAGATATGCTAGCTGCTGAAGGTACCCCTTACAAAGTGGGTCCAGTTCC 559
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 754 ATGATTTAGAGTACGCGCTGCGTGGCGCCGCCGCTCCCGGTAGACAGACTTCC 813
OY 560 TCAAGATCTAAAGATTGATAGAAAGACAGCAATTCATATATGGGAAGCCAGTGA 619
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 814 TACAGACCTCAAGCAATTTGGTGAAGAAAGCTAGAGCAAGCAAGAGAAAGCCAGTGA 873
OY 620 TACTTCTCTCCACAGATTAGAGAGCGCTATTGCTTACAGTCAATTAATAAGAACCCCC 679
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 874 TACTCTCTCCCATAGCCCTAGGAGAGACTTTCTCTCCATTTCCCAACCGTACGACCC 933
OY 680 CCTCTTGGCGCAAAAAATTCATCAACACTTTCATTCCTTTTCAGCTCCAGTGGGTG 739
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 934 CTTCATGCGCGCGCAAGTACATCAAACTTTGTTGCTACCTCCGCGCCATGGGGTG 993
OY 740 CTATAGACAAATGTACACTTTGCTGTCGCAACACTTTGGGAGTCCCTAGTGGACC 799
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 994 CGATCTCTCAGATGAGACATTTGCTTGGCAACACACTCGGTGCTCCCTTTAGTTAAC 1053
OY 800 CTTTATTAGTGGAGATGAACAAGAGCTCCGAGATGACCTTTGGCTTTGCGCTAAC 859
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1054 CTTTGTGCTGTCAGACCGCATTCAGAGAGACTCCGAGAGTAAACCAATGCTACTTCCATCTA 1113
OY 860 CAAAAATTTTGGTCTCTCAA---AAACAATAGTGAATTAACCTCAATTTAGCCCTTATTCAG 916
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1114 CCAAAAGTTTTCACGACAGCACTAAACCGCTTGTCTACTCCGCCAGTGTAACTACACAG 1173
OY 917 CTCATGACATGTTGATTTTCTTAAAGACATTTGCTTTCTGTAAGGGGTTTATCTTATG 976
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1174 CTTCACGAGTGGATCGGTTTTTTCAGACATTTGATTCACAAAGAGTTTGTGCTTTACA 1233
OY 977 AAACAGAAATTTACCTGATAGGAGACATTAAGCAGACAGACAGAGGCTTAACTATGTA 1036
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1234 AGACAAAGATGTTGCTTTTAAACAGAGAGCTGATGACTCCGGGAGTCCAGTACACTTGA 1293
OY 1037 TTTATGGGAAGGAGTGGGAACTTTGTAATGTTATGGAAGGTGATTTTGTATG 1096
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1294 TTTATGGGAGAGATTTGATACCGGAGTTTGTATGATGAAAGAGAGATTCGTATGA 1353
OY 1097 AACGGCCAAATATCATCTATGCGGATGCGTGAACGGTGAACCTTGGTACTTGTGG 1156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1354 ACCAACCAAGAGATTAAGTATGGAGATGGAGCGGTTAATTTGGGAGACTTAAAGCAG 1413
OY 1157 CGCTTCAATCACTATGAAAGAGAGAAATCAATACCTTAAAGGTGTAAGCTATGATG 1216
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1414 CTTT-----GAAAGTGCATAGCTTTGAACACCGGTAGAGATTGATG 1452
OY 1217 GGGTGTCTCATCTCAATCACTTAAGAGATGAAGTTGCACATAAATAGTAGTGAGA 1276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1453 GAGTTTCCGATACATCTATTAAGAAAGAGAGATGCGACTTAAAGGATTATGAAGCAGA 1512
OY 1277 TTTACTCAATTAATTTCTCA 1295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1513 TTTCAATTAATTAATTAATGA 1531

```

RESULT 8

AA501087 standard; cDNA: 264 BP.

AA501087:

31-MAY-2001 (first entry)

Soybean sterol acyltransferase LCAT EST sequence #1.

```

XX Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
KW acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
KW nutritional supplement; dairy product; food product; salad dressing;
KW soybean; Arabidopsis thaliana; expressed sequence tag; EST; ss.
XX
OS Glycine max.
DB WO200116308-A2.
XX
PN 08-MAR-2001.
XX
PD 30-AUG-2000; 2000MO-US23863.
XX
PR 30-AUG-1999; 99US-0152493.
XX
PA (MONS ) MONSANTO CO.
XX
PI Lassar M, Van Benennaam A;
XX
PS WPI, 2001-169010/17.
XX
PT New isolated nucleic acid encoding plant lecithin:cholesterol
PT acyltransferase-like or acyl (coenzyme A) CoA:cholesterol
PT acyltransferase-like polypeptides, for modifying the sterol content and
PT oil production of plants -
XX
PS
XX
XX Claim 5; Page 86; 127pp; English.
XX
CC The present sequence for soybean LCAT (lecithin:cholesterol
CC acyltransferase-like) EST sequence #1 is closely related to the
CC Arabidopsis thaliana LCAT1 sequence. Several novel polynucleotides
CC encoding the plant sterol acyltransferases LCAT (AA501081-AA501104,
CC AA501341) and ACAT (acyl CoA:cholesterol acyltransferase-like;
CC AA501311-AA501319) are described. A yeast LCAT related open reading
CC frame, LK01 gene sequence (AA501342), and a rat ACAT (AA501105) cDNA
CC sequence are also described. The polynucleotides encoding LCAT or ACAT
CC are used to produce LCAT or ACAT polypeptides. They can also be used in
CC a recombinant construct to transform a host cell (preferably of a plant)
CC or a plant. The recombinant construct is used to increase or decrease
CC the sterol content of the host cell or plant. It can be used to alter
CC oil production of the cell or plant, preferably by increasing it. The
CC oil of the plant or the plant itself is used as a food product, or as
CC nutritional or dietary supplements, or in pharmaceutical compositions
CC for lowering cholesterol. The oil can be used in foods e.g. margarine,
CC butter, cooking oil, and dressings e.g. salad dressings, mayonnaise,
CC cheese, processed meat, pasta, sauces, cereals, desserts, dips, chips,
CC baked goods, pastries, cookies, snack bars, confections, chocolates, and
CC beverages. The alteration in sterol content and/or composition can also
CC provide a plant with tolerance to stress and insect damage.
XX
XX Sequence 264 BP; 62 A; 73 C; 52 G; 74 T; 3 other;
XX
XX
XX Query Match 18.7%; Score 249; DB 22; Length 264;
XX Best Local Similarity 98.5%; Pred. No. 5e-64;
XX Matches 260; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
OY 315 CCAGAACATCGATGATTAATTCACACGCTCGGGTGGAGACCGGGTCCCTACCTTGG 374
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 CCAAGACATCGATGATTAATTCACACATCTCTGGGTTGAGACCCGGGTCCCTACCTTGG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 375 TTTCACCAACTCTCTTCT-ATCTCAATCTCTCTCAAGCATATCAACCGATATCATG 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 TTTCACCAACTCTCTTCTCTCATCTCATTCATCCGTCCTCAAGCATATCAACCGATATCATG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 434 CACCCCTGTAGATTCATTACAAAGCTTGGCTACGCTGATGATGAGACTCTGTTGGAG 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CACCCCTGTAGATTCATTACAAAGCTTGGCTACGCTGATGATGAGACTCTGTTGGAG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 494 CCCCTTATGACTTTAGATATGCTAGCTGCTGAAGGTACCCCTTCAAGGTGGTCCA 553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 CCCCTTATGACTTTAGATATGCTAGCTGCTGAAGGTACCCCTTCAAGGTGGTCCA 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 554 AGTCTCTCAAGATCTAAGAATT 577
 |||||
 Db 241 NGTCTCTCAAGATCTAAGAATT 264

RESULT 9
 AAA49204
 ID AAA49204 standard; cDNA; 1500 BP.
 XX
 AC AAA49204;
 XX
 DT 12-DEC-2000 (first entry)
 XX
 DE Corn putative lecithin:cholesterol acyltransferase gene #4.
 XX
 KW Corn; lecithin:cholesterol acyltransferase; phytosterol;
 XX phosphatidylcholine-sterol O-acyltransferase; heat shock; cold shock; ss.
 OS
 XX Zea mays.
 FH Key Location/Qualifiers
 FT 24..1277
 FT CDS /*tag= a
 FT /product= "lecithin:cholesterol acyltransferase"
 FT /EC_number= "2.3.1.43"
 XX
 PN M0200032791-A2.
 XX
 XX 08-JUN-2000.
 PD
 XX 02-DEC-1999; 99WO-US28586.
 PF
 XX 03-DEC-1998; 98US-0110782.
 PR
 PA (DUP0) DU PONT DE NEMOURS & CO E I.
 PA Cahoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;
 XX WP1: 2000-412337/35.
 DR P-PSDB; AAB01209.
 XX
 XX Polynucleotide encoding plant lecithin:cholesterol acyltransferase
 PT enzyme useful for producing transgenic plants and for producing
 PT antibodies specific to which is useful for screening cDNA expression
 PT libraries
 XX
 PS Claim 2; Page 41-42; 49pp; English.
 XX
 CC The present sequence is a putative coding sequence for a corn
 CC lecithin:cholesterol acyltransferase (also known as
 CC phosphatidylcholine-sterol O-acyltransferase). This enzyme is found
 CC associated with high-density lipoproteins and Apolipoprotein-AI and -D.
 CC The gene and protein can be used to produce transgenic plants which have
 CC increased lipid metabolism and membrane fluidity, and therefore increased
 CC resistance to heat and/or cold shock, to alter the content of phytosterol
 CC or lecithin in grains and to identify potential herbicides.
 CC
 XX Sequence 1500 BP; 304 A; 469 C; 454 G; 271 T; 2 other;
 SQ

Query Match 15.6%; Score 208; DB 21; Length 1500;
 Best Local Similarity 51.9%; Pred. No. 2e-51;
 Matches 516; Conservative 1; Mismatches 472; Indels 6; Gaps 2;

QY 283 TGCTTTGCCGAACGATGACCTTCATTACACCAAGATCGATGATTACTTCAACACT 342
 |||||
 Db 273 TGTTTCGCCGAGAGATGCGCAGCGCGTACGACGCGGCTCCGACTACCGCAAGCC 332

QY 343 CCTGGGGTTGAGACCCGGGTCCTTACCTTGTGTTCCACCAACTCTCTTCTATCTCAAT 402
 |||||
 Db 333 CAGGCGGTGGAGACCCGGGTCCTTCTTGTGATCACCAGCGGCTTCGCTACCCGAC 392

QY 403 CCTGCTCAAGCATATACCGGATACGACCCCTGTAGATTCAATCAAAAGCTT 462
 |||||

Db 393 CCAGACCCGGAGAACTTCTCTCT---GTACATGACAAAGTTCTGTCGCGGCTGGAGGCGCTC 449
 QY 463 GGCTACGCTGATGTGAACACTCTGTTGGAGCCCTTATGACTTATGATATGTTACT 522
 |||||
 Db 450 GCGTACCCGCGAGCGGCAACCTGTTGCGCGCGCCCTACGACTTCGGGTACGCCCTGCC 509

QY 523 GCTGAAGGTACCCCTTCACTCAAGTGTCCAAAGTTCCTCAAAAGATCTAAAGATTGTGTA 582
 |||||
 Db 510 CCGCCAGGCGACCGCTCGAGGCTCGCNGACCGCTTCTTGGGCGCCTCAGAGGGCTGGTA 569

QY 583 GAAGAAGCAAGCAATTCATATATGGAAGCCAGTATCTTCTCCACAGTTTATGA 642
 |||||
 Db 570 GAGAGGGGAGAGCGGCTTAAGGAGAGGCGCGTACACCTGCGGCGACAGCTACAGG 629

QY 643 GGCTATTGTTCTCAACTACTAATAGAAACCCCTCTTGCGCGCAAAAATTCAATC 702
 |||||
 Db 630 GGCACGGTGGGCGCACCACTTCTTCTGCGGCGCCCTTGCGGCGAGCGCTTCTGTC 689

QY 703 AAACACTCATTTGCTCTTCAAGCTCCATGGGCTGGCTATAGAGAAATGTACCTTT 762
 |||||
 Db 690 CGGCGGTTGTCGCCGTTGCGCGCTGGGAGGCGTCTGCTTGGCATGCTGCAATC 749

QY 763 GCATCTGGCAACACTTTGGAGTGCCTTAGTGACCTTTATATGAGGAGATGAAACA 822
 |||||
 Db 750 GTGCGCGGCAACATCTGGGCTGCGCTTCTGCGACCGCGTGGCGCTCAAGGCGAGTAC 809

QY 823 AGAAGCTCCGAGAGTAACTTTGGCTTTGCTTAACCCAAAATTTTGGTCTTAAAAA 882
 |||||
 Db 810 CGGACCTGACAGAGAGCTCTGGCGCGCTGCCAACCCCAACGCAATTTAGAGCCGCGGAG 869

QY 883 CCAATAGATATACATTCATTAATGAGCTTATTCAGCTCAAGATGATGATTTCTAAAA 942
 |||||
 Db 870 CCATGTTGACCAACAGGAGACGACGTACACGCGCCACGACATGCGGACTTCTCGAC 929

QY 943 GACATTGTTTTCTGAAGGGGTTATCTTATGAAACGAAATCTACCTTTGATAGG 1002
 |||||
 Db 930 GGCATCGGGCTAGGCGGCAATTTGCGGTACGATGCCGCGTCCGCTGCTGCTGCGG 989

QY 1003 AACATTAAGACACACAAAGTCTTAACTGTATTTATGGAACGAGAGTGGAACTTG 1062
 |||||
 Db 990 GAGCTGCCATCTCCGCGGCTGCCCTGTGTGTGCTGGGGTGGCTGGACACGCCG 1049

QY 1063 GAAACATTTGTTTATGGAAGGATTTTATGTAAGCGCCGAAATATCATATGGGAT 1122
 |||||
 Db 1050 GAGATGCTGGCTTACCCGAGACGACTTGCAGGACCGGATGATGTCTATGGAGAC 1109

QY 1123 GGTGATGGAACGCTGAACCTTGGTGAAGTGTGCGCTTCAATCACTATGGAAGAGG 1182
 |||||
 Db 1110 GCGGACGGGCTGTCAACCTGTTGAGCTCTCGCTGTGACACCTGCGTGGAGGCTTCT 1169

QY 1183 AAAAATCAATACCTTAAAGTGTATAGATAGATGGGGTGTCTCAATCTTCAATTAAG 1242
 |||||
 Db 1170 ACAGCT---TACTTTAGATGCTCAAGGTGCGCAACGTTGTACACACGGGCTCTTCTG 1226

QY 1243 GATGAAGTTCACATAAGTAATAGTAGTGGAT 1277
 |||||
 Db 1227 GAGGATGCTGCTCGCGTTATTCATTAAGCGCAT 1261

RESULT 10
 AAS01088
 ID AAS01088 standard; cDNA; 273 BP.
 XX
 AC AAS01088;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Soybean sterol acyltransferase LCAT EST sequence #2.
 XX
 KW lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
 KW acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
 KW nutritional supplement; dairy product; food product; salad dressing;
 KW soybean; Arabidopsis thaliana; expressed sequence tag; EST; ss.

XX Cahnou RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;
PI WPI: 2000-412337/35.
XX P-PSDB: AAB01205.
XX
PT Polynucleotide encoding plant lecithin:cholesterol acyltransferase
PT enzyme useful for producing transgenic plants and for producing
PT antibodies specific to which is useful for screening cDNA expression
PT libraries
XX
PS Claim 2: Page 35-36; 49pp; English.
XX
CC The present sequence is a putative coding sequence for a corn
CC lecithin:cholesterol acyltransferase (also known as
CC phosphatidylcholine-sterol O-acyltransferase). This enzyme is found
CC associated with high-density lipoproteins and Apolipoprotein-A1 and -D.
CC The gene and protein can be used to produce transgenic plants which have
CC increased lipid metabolism and membrane fluidity, and therefore increased
CC resistance to heat and/or cold shock, to alter the content of phytosterol
CC or lecithin in grains and to identify potential herbicides.
XX
SQ Sequence 542 BP; 84 A; 179 C; 181 G; 90 T; 8 other;

Query Match 7.9%; Score 105; DB 21; Length 542;
Best Local Similarity 53.5%; Pred. No. 6, 9e-21;
Matches 219; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

OY 629 CCACAGTTAGAGGCGCTATTTGCTTACACTACTAATAAAGAACCCCTCTTGGC 688
DB 5 CGCACGCTACGCGCGGCGACGCTGGCGCACCACTTCTACTGCGCGCGCTTGCCTGGC 64
OY 689 GCAAAAATTCATCAAAACATTCATTTCTTCAAGCTCCATGGGGTGTATAGAG 748
DB 65 GCAGCGGCTTCGTCGCGGGTTCGTGCTGCGGCGACCGTGGGAGGCGTCTCTTG 124
OY 749 AATGTACACCTTTGATCTGGACACTTTGGGAGTCCCTAGTGCACCTTATTAG 808
DB 125 GCATCGTCAATCGTCGCGCGGCAACATCTCGGCTTCTGCTGCGACGCGTGGCG 184
OY 809 TGAGGATGAACAAAGAACCTCGAGAGTAACTTGGCTTTCCTAATCCCAAAATTT 868
DB 185 TCAGAGGCGAGTACGCGAGCTTCGACAGCACTCTGGCGCTGCCCAACCCCAAGCAT 244
OY 869 TTGGTCTCTAAAACCAATATGATATCAATTAAGGCTTATTCAGCTCATGACATG 928
DB 245 TTAGAGCGCGGACGACGCTGTGACACAGGAGGAGGAGTACAGCGCCAGACATGG 304
OY 929 TTGATTTTCTAAAAGACATTTGTTTCTGAAAGGGTTTATCTTATGAACACGATTG 988
DB 305 CGGACTTCTCGACGCAATGAGGCGCAATTTGTGCGGTAACGATCCCGCGTGC 364
OY 989 TACCTTGTAGGAACATTAAGACACCAAGTGCTTAACTTGTAT 1037
DB 365 TCCCTCTGTTCCGGAGCTGCATCTCCGCGGTGCTGCTGTGT 413

RESULT 14

AAAA9205
ID AAAA9205 standard: cDNA; 1660 BP.

XX AAAA9205;

DT 12-DEC-2000 (first entry)

XX Corn putative lecithin:cholesterol acyltransferase gene #5.

KM Corn; lecithin:cholesterol acyltransferase; phytosterol;
XX phosphatidylcholine-sterol O-acyltransferase; heat shock; cold shock; ss.

OS Zea mays.

XX key Location/Qualifiers

FT CDS 77..1396
FT /*tag= a
FT /product= "lecithin:cholesterol acyltransferase"
FT /EC_number= "2.3.1.43"

PN WO200032791-A2.

PD 08-JUN-2000.

PF 02-DEC-1999; 99WO-US28586.

PR 03-DEC-1998; 98US-0110782.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Cahnou RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;

DR WPI: 2000-412337/35.

XX P-PSDB: AAB01210.

PT Polynucleotide encoding plant lecithin:cholesterol acyltransferase
PT enzyme useful for producing transgenic plants and for producing
PT antibodies specific to which is useful for screening cDNA expression
PT libraries

XX Claim 2: Page 43-44; 49pp; English.

CC The present sequence is a putative coding sequence for a corn
CC lecithin:cholesterol acyltransferase (also known as
CC phosphatidylcholine-sterol O-acyltransferase). This enzyme is found
CC associated with high-density lipoproteins and Apolipoprotein-A1 and -D.
CC The gene and protein can be used to produce transgenic plants which have
CC increased lipid metabolism and membrane fluidity, and therefore increased
CC resistance to heat and/or cold shock, to alter the content of phytosterol
CC or lecithin in grains and to identify potential herbicides.

XX Sequence 1660 BP; 361 A; 475 C; 499 G; 325 T; 0 other;

Query Match 7.2%; Score 95.4; DB 21; Length 1660;
Best Local Similarity 46.9%; Pred. No. 8, 8e-18;
Matches 574; Conservative 0; Mismatches 606; Indels 45; Gaps 7;

OY 95 GGGCAAGCACTCGACCTTGTATTAATACAGTACGAGGAGGAACCACTAGAG 154
DB 177 GCGCAACAACCTTCCACCCATCTTGTGTAGTGGGTGAGCGACGCTGGAG 236
OY 155 CAAGGTGACCAATAGTCAAGCCCTTACTTATCTGCGCAATCATGTACCTTCA 214
DB 237 CACGCTTACCGAGAGTACCGCGCTGCTGCCGACTGC-----GCG 281
OY 215 TCAGAAAAAAGATGATGTTTCAAGCTTGGTATTCAGTGTCACTTACTTGTCT 273
DB 282 CGATGAAGGGAAGGGGTGTCTGTGTGTGAAGAAGTTCGAGTGTCTGTCTG 341
OY 274 --TTCACTCAATGCTTGGCGGAAGCATCCCTTCAATTAACCAAGAAGTGTAT 331
DB 342 ACTAGTGCAGTGTCTGAGAGAGATGAGCTGTCTGACACCTCGCATCAAGAGT 401
OY 332 ACTTCAACACCTCTGGGTGAGACCGGCTCCATCTTGTGTTCCCAACTCTCTTC 391
DB 402 ACCGGAACCTCGCGGCGAGACGCGATGCCAATCTGGCTCCCAAGAAGCTTCA 461
OY 392 TCTATCTCAATCTCGTCAAGCATATACCGGATATGACGACCCCTGTAGATTGAT 451
DB 462 GCCACAAGAACCCCTCAAGTCAGA-----CTGTTGCTCGGAAGAGTGAAGCCGAC 515
OY 452 TACAAAAGCTTGGCTACGCTGATGTGAGACTCTGTGGAGCCCTTATGACTTTAGAT 511
DB 516 TGGAGACATGGATACGAGACGAGACACCATGTTCGAGACCCCTTACGACTTCCGT 575
OY 512 ATGCTCTAGCTGTCAAGGTCACTTCAAGTGGGTTCGAAGTTCCTCAAGATCTAA 571
DB 576 ACGCGCGCGCTCCCGCGCAGAGCTCGAGGTGTACTCCGCTACTTCAAGAGAGCTGA 635

[illegible]

FT	/partial	
XX	/Ec_number=	"2.3.1.43"
XX	WO200032791-A2.	
XX		
XX	08-JUN-2000.	
XX		
XX	02-DEC-1999;	99WO-US28586.
XX		
XX	03-DEC-1998;	98US-0110782.
XX		
XX	(DUPO) DU PONT DE NEMOURS & CO E. I.	
XX		
XX	Cahoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JT;	
XX	WPI; 2000-412337/35.	
XX	P-PSDB; AAB01206.	
XX		
XX	Polynucleotide encoding plant lecithin:cholesterol acyltransferase	
XX	enzyme useful for producing transgenic plants and for producing	
XX	antibodies specific to which is useful for screening cdna expression	
XX	libraries	
XX		
XX	Claim 2; Page 36-37; 49pp; English.	
XX		
XX	The present sequence is a putative coding sequence for a corn	
XX	lecithin:cholesterol acyltransferase (also known as	
XX	phosphatidylcholine-sterol O-acyltransferase). This enzyme is found	
XX	associated with high-density lipoproteins and Apolipoprotein AI and	
XX	The gene and protein can be used to produce transgenic plants which h	
XX	increased lipid metabolism and membrane fluidity, and therefore increas	
XX	resistance to heat and/or cold shock, to alter the content of phytos	
XX	or lecithin in grains and to identify potential herbicides.	
XX		
XX	Sequence 921 BP; 176 A; 300 C; 280 G; 164 T; 1 other;	
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XX	Query Match	6.5%; Score 86.4; DB 21; Length 921;
XX	Best Local Similarity	51.3%; Pred. No.3.2e-15;
XX	Matches 319; Conservative	0; MisMatches 276; Indels 27; Gaps
XX		
XX	95 GGGCAAGCAACCTCGACCCCTTGATTCTCAATACCAAGCAAGGAGGCAACCACTAGAG	15
XX	170 GGGCCAAACACTTCCACCCACTTTCGTGAGCTGGGGGTAGCTGACGCAACCTGGAGG	22
XX	155 CAGGCTTGACCAATCACTAGACAAGCCCTCTACTTTCATTTGGCAATCAATGTAACCTCTCA	214
XX	230 CACGGCTCACCAGGAGATACCGCGCGCTGGTCCGCAATGG-----CGG	27
XX	215 TCAGAAAAAGAAATGATGTTGACAGCTTGGTTCATTCAGTGTCTACTTCTCTCT- 27	
XX	275 CCATGAAGGGAGGAGGGGTGTGGTGTGTGGAAAGACATTCGGAGCTGCTGTCTGTG	334
XX	274 --TTCACTCAATGCTTTGCCAAGCAGATGACCTTCATTTACCACCAAGAACTCGATGATT	333
XX	335 ACTAGCTGAGAGCTTCAGGAGAGCAAGATGAGCCTCTGTACGACCTCTCCATCAACGAGT	394
XX	332 ACTTCACACCTCTGTGGGGTTGAGACCCGGGTCCTCACTTTGGTTCACCAACTCTCTC	393
XX	395 ACCGGAACCTCGCGCGCTCGAGAGCGCAAGTGTCCCACTTGGCTTCACCAAGACCTTCA	455
XX	392 TCTATCTCAATCTGTCTCAAGCATATCACCGGATACATGGCAACCCCTGGTAGATTGAT	453
XX	455 GCCACAGAACCCCTCAAGTCAAG-----CTGGTGCCTCGGAAGGCTGAGAGCGGAC	508
XX	453. TCAAAAGCTTGGCTAGCGTGTATGCTGAGACTGTCTTTGGAGCCCTTATGACTTTAGAT	511
XX	509 TGGAGAGACATGGGATACCGAGACGAGACACCATGTTCTGGAGCCCTTCACACATTCGCT	566
XX	512 ATGAGCTAGCTGCTCAAGGTACACCTTCACAAGGAGGTTCAAGTCTCTCAAAAGCTAA	573
XX	569 ACGCGCGCGCTGCGCGCGCGAGCTGCGAGGTGTACTCCCGCTACTTCAAGAGAGCTGA	622
XX	572 AGAATTTATAGAGAACGACAAATTCATTAATGGCAACCCAGTGTACTTCTCTCC	631

Db 629 TGGAGCTGGTCCGAGGCGCGAGAGAGACC CGGAAGAAGCGCTCATC--CTCGGCC 685
Qy 632 ACAGTTTAGGAGGCGCTATTGTCCTACAACTACTAAATAGAAACCCCTCTTGGCGCA 691
Db 686 ACAGCTTGGCGCGCATGTCGCGCTCGAGTTCGCCGAACACTCCGCCGCGTGGCGGC 745
Qy 692 AAAAATTGATCAAAACACTTCAT 713
Db 746 GCGAGCACATCGAGCGCGCTCGT 767

Search completed: February 15, 2003, 12:05:21
Job time : 231 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:01:27 : Search time 54 Seconds
(without alignments)
7564.693 Million cell updates/sec

Title: US-09-857-612A-13
Perfect score: 1332
Sequence: 1 atgaagaagaagaagaaga.....gtatttgcgcgggttaa 1332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_MA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCrUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46.4	3.5	7218	1	US-08-232-463-14 Sequence 14, Appl
2	45	3.4	7218	1	US-08-232-463-14 Sequence 14, Appl
3	37.6	2.8	3581	2	US-08-738-349-1 Sequence 1, Appl
4	36.8	2.8	1776	3	US-08-655-352-10 Sequence 10, Appl
5	36.8	2.8	1776	4	US-09-258-016-10 Sequence 10, Appl
6	36.8	2.8	1776	4	US-09-257-825B-10 Sequence 10, Appl
7	33.8	2.5	3095	6	5231168-1 Patent No. 5231168
8	33.4	2.5	981	4	US-09-134-001C-982 Sequence 981, App
9	32.6	2.4	2402	4	US-09-221-017B-881 Sequence 1, Appl
10	32.4	2.4	5943	1	US-08-206-176-1 Sequence 1, Appl
11	31.6	2.4	2263	2	US-08-687-865A-1 Sequence 1, Appl
12	31.6	2.4	2263	4	US-09-043-711-1 Sequence 1, Appl
13	31.6	2.4	50000	4	US-09-146-053-4 Sequence 4, Appl
14	31.4	2.4	2845	1	US-08-289-653-1 Sequence 1, Appl
15	31.4	2.4	4822	4	US-09-484-970B-106 Sequence 106, App
16	31.4	2.4	5785	3	US-08-480-640A-221 Sequence 221, App
17	31.4	2.4	5785	4	US-08-686-968C-221 Sequence 221, App
18	31.4	2.4	5785	4	US-08-488-237A-221 Sequence 221, App
19	31.2	2.3	1026	4	US-09-134-001C-660 Sequence 660, App
20	31.2	2.3	1960	4	US-09-280-116-133 Sequence 133, App
21	31.2	2.3	3763	1	US-07-792-865D-1 Sequence 1, Appl
22	30.8	2.3	35828	4	US-09-449-218D-17 Sequence 17, Appl
23	30.6	2.3	1866	4	US-08-936-165A-202 Sequence 202, App
24	30.6	2.3	1950	4	US-09-134-001C-1054 Sequence 1054, App
25	30.6	2.3	16593	4	US-08-961-527-52 Sequence 52, Appl
26	30.6	2.3	30549	4	US-09-134-001C-322 Sequence 322, App
27	30.4	2.3	3541	4	US-09-180-439-5 Sequence 5, Appl

28	30.4	2.3	3979	4	US-09-180-439-1 Sequence 1, Appl
29	30.4	2.3	3979	4	US-09-180-439-2 Sequence 2, Appl
30	30.4	2.3	4123	4	US-09-180-439-7 Sequence 7, Appl
31	30.4	2.3	4746	2	US-08-819-288-2 Sequence 2, Appl
32	30.4	2.3	4746	4	US-09-400-348-2 Sequence 2, Appl
33	30.4	2.3	4747	4	US-08-261-822A-2 Sequence 2, Appl
34	30.4	2.3	4747	5	PCT-US95-07744A-2 Sequence 2, Appl
35	30.4	2.3	6042	4	US-08-261-822A-1 Sequence 1, Appl
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37	30.4	2.3	6172	2	US-08-819-288-1 Sequence 1, Appl
38	30.4	2.3	6172	4	US-09-400-348-1 Sequence 1, Appl
39	30.2	2.3	369	4	US-09-134-001C-177 Sequence 177, App
40	30.2	2.3	452	4	US-09-221-017B-146 Sequence 146, App
41	30.2	2.3	732	4	US-09-134-001C-124 Sequence 124, App
42	30.2	2.3	1958	2	US-08-390-888A-1 Sequence 1, Appl
43	30	2.3	2877	4	US-09-619-353-1 Sequence 1, Appl
44	29.8	2.2	1563	4	US-09-177-249-3 Sequence 3, Appl
45	29.8	2.2	3222	4	US-08-936-165A-111 Sequence 111, App

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHERFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
CLASSIFICATION: 435
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-Fls
US-08-232-463-14
Query Match 3.5%, Score 46.4, DB 1, Length 7218;

Best Local Similarity 6.28; Pred. No. 0.0002;
Matches 23; Conservative 192; Mismatches 153; Indels 0; Gaps 0;

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Oy 909 TTTATGAGTCATGACATGTTGTTTCTTAAAGACATTGTTTCTGGAAGGGTTTA 968
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Db 1479 TTACCTATCTATGCAAGTACTTAAAGATAGAGAAATTGGACRRTTTRTTRTTR 1420
Oy 969 TCCTATGAACAGCAATCTACCTTGTATAGGAACATTAAGACCAACAGCTGCTAT 1028
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Db 1419 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1360
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    : : : : : : : : : : : : : : : : : : : : : : : : : :
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Oy 1089 TTTTGTGAACGGCCAGAAATATCATATGGGATGGATGGAAGCTGCTGATG 1148
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Db 1299 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1240
Oy 1149 CTTGTGGCGCTTCAATCATATGAAAGAGAGAAATCAATACCTTAAAGCTTAA 1208
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Oy 1209 GATAGTGGGGTGTCTCATCTACTTAAAGATGGAAGTGCCTAATAGT 1268
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Oy 1269 AGGTGAGA 1276
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RESULT 2

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US-08-232-463-14
: Sequence 14, Application US/08232463
: Patent No. 5670367
: GENERAL INFORMATION:
: APPLICANT: DORNER, F.
: APPLICANT: SCHEIFLINGER, F.
: APPLICANT: FALKNER, F. G.
: TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 1800 Diagonal Road, Suite 500
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22313-0299
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232.463
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/935.313
: FILING DATE:
: APPLICATION NUMBER: EP 91 114 300.6
: FILING DATE: 26-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: BENT, Stephen A.
: REGISTRATION NUMBER: 29,768
: REFERENCE/DOCKET NUMBER: 30472/114 IMMU
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703)836-9300
: TELEFAX: (703)683-4109
: TELEX: 899149
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:

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: LENGTH: 7218 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: CLONE: pTZ9pt-FLS
US-08-232-463-14

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Query Match 3.4%; Score 45; DB 1; Length 7218;
Best Local Similarity 5.8%; Pred. No. 0.00057;
Matches 24; Conservative 212; Mismatches 177; Indels 0; Gaps 0;

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Oy 180 CTCCTACTTCATCTGGCAATCATGTACCCCTCATCAAGAAAGATGATGTTTCAG 239
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1067 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1126
Oy 240 ACTTTGGTTGATTCAGAGTCACTACTGCTCTTCACTCAATGTTTGGCAAGCAT 299
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1127 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1186
Oy 300 GACCCCTTCAATACACCAAGACTCGATGATTAATCACTCAACACTCGGGGTTGAGACCCG 359
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1187 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1246
Oy 360 GGTCCCTCACTTGTGTCACCAACTCTCTCTATCTCAATCTCTGTCAGCATAT 419
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1247 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1306
Oy 420 CACCGATACATGCGACCCCTGTGATTCATTCATTAACAAGCTTGGTACGCTGATGTGA 479
    : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1307 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1366
Oy 480 GACTCTGTTGGAGCCCTTATGACTTGTAGATATGCTAGCTGGAAGTCACCCCTTC 539
    : : : : : : : : : : : : : : : : : : : : : : : : : :
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Oy 540 ACAAGTGGTTCACACTCTCAAGATCTAAGATTTGATAGAGAACAA 592
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Db 1427 YYYYYYGTACCAAAATCTCTATCTCTTTAACTACTTGCATAGATAGTAA 1479

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RESULT 3

```

US-08-738-349-1/C
: Sequence 1, Application US/08738349
: Patent No. 5869638
: GENERAL INFORMATION:
: APPLICANT: Takeshita, Sunao
: APPLICANT: Okazaki, Makoto
: APPLICANT: Kawai, Shinji
: APPLICANT: Tsujimura, Atsushi
: APPLICANT: Amann, Egon
: TITLE OF INVENTION: Bone-Related Cadherin-like Protein and
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
: STREET: 1300 I Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/738.349
: FILING DATE: 25-OCT-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/364.439

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FILING DATE: 08/11/2001
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
STRAIN: osteoblastic cell line MC3T3E1
FEATURE:
NAME/KEY: CDS
LOCATION: 284..2671
US-08-738-349-1

Query Match
Best Local Similarity 50.6%; Score 37.6; DB 2; Length 3581;
Matches 91; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Db 1129 GGAACGGTGAAGCTGTGAGCTGTGGCGCTTCATCACTATGAGAGAGAGAAAT 1188
1129 GGAACGGTGAAGCTGTGAGCTGTGGCGCTTCATCACTATGAGAGAGAGAAAT 1188
Db 3070 GAACCTGTGCTTCTTAATTTTGTGAGAGCTCTTTCAGCAATTAATAAATTAAG 3011
3070 GAACCTGTGCTTCTTAATTTTGTGAGAGCTCTTTCAGCAATTAATAAATTAAG 3011
Qy 1189 CAATACCTTAAGGTTAGATAGATGGGTCTCATCTTAATTAAGATGAA 1248
1189 CAATACCTTAAGGTTAGATAGATGGGTCTCATCTTAATTAAGATGAA 1248
Db 3010 AGACAGCTTAGGTTCTTAACACATAGACGATTTCCCTTCATTTAGATTACCGTGAC 2951
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Qy 1249 GTTGCACTTAATGAATAGTAGAGATTCATTAATTCATTCATGCTGAGCTGCT 1308
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Db 2950 TTCTCCTTCAATTAATATTTTGTGTCAGCAAGTGCTTTTCTTCTACTGAAGTTGAT 2891
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RESULT 4
US-08-655-352-10/c
Sequence 10, Application US/08655352
Patent No. 6077991
GENERAL INFORMATION:
APPLICANT: Bachettira W. Pooviah, Zhilua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449

FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: Tobacco CcAmk cDNA and deduced amino-acid
SEQUENCE:
FEATURE:
NAME/KEY: protein-coding sequence (not including
stop codon)
LOCATION: nucleotides 20-1570
US-08-655-352-10

Query Match
Best Local Similarity 56.7%; Score 36.8; DB 3; Length 1776;
Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 1074 TTATGGGAAGGCTATTTGATGAGCGCCAGAAATATCATATGAGGATGATGACAC 1133
1074 TTATGGGAAGGCTATTTGATGAGCGCCAGAAATATCATATGAGGATGATGACAC 1133
Db 1703 TTAATTTAAAGACCTTTTTCAGTAGATGATTAATAAATATGATGTCTAGANA 1644
1703 TTAATTTAAAGACCTTTTTCAGTAGATGATTAATAAATATGATGTCTAGANA 1644
Qy 1134 GGTGACCTGGTGAAGCTGTGAGCGCTTCATCACTATGAGAGAGAGAGAAATTCATA 1193
1134 GGTGACCTGGTGAAGCTGTGAGCGCTTCATCACTATGAGAGAGAGAGAAATTCATA 1193
Db 1643 GTTAGAGATTAATAGATAGATGCGGTATTATTAATAAAGAGCAAAATTCATA 1584
1643 GTTAGAGATTAATAGATAGATGCGGTATTATTAATAAAGAGCAAAATTCATA 1584

RESULT 5
US-09-258-016-10/c
Sequence 10, Application US/09258016
Patent No. 6362395
GENERAL INFORMATION:
APPLICANT: Bachettira W. Pooviah, Zhilua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,016
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stephens Jr., Donald L.
REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-51994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: Tobacco CCAK CDNA and deduced amino-acid
DESCRIPTION: sequence
FEATURE:
NAME/KEY: protein-coding sequence (not including
NAME/KEY: stop codon)
LOCATION: nucleotides 20-1570
US-09-258-016-10

Query Match 2.8%; Score 36.8; DB 4; Length 1776;
Best Local Similarity 56.7%; Pred. No. 0.11;
Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
OY 1074 TTATGGGAAGGTGATTTTGATGAACGCCAGAAATATCATATGCGGATGCGATGGAAC 1133
DB 1703 TTAATTTAAAGGATCTTTTACGAGTAGATATAAATATGATGATGAGAA 1644
OY 1134 GGTGAAGTGGTGGCTTGGCGCTTCATCATGTAAGAAAGGAGAAATCAATA 1193
DB 1643 GTTAGAGATATTAAATGAAATAGCGTGTATTCAAAATTAAGAGCAAAATTCATA 1584

RESULT 6
US-09-257-825B-10/C
Sequence 10, Application US/09257825B
Patent No. 6403352
GENERAL INFORMATION:
APPLICANT: Pooviah, Bachettira W.
APPLICANT: Patil, Shameekumar
APPLICANT: Takezawa, Daisuke
TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
FILE REFERENCE: 4630-51993
CURRENT APPLICATION NUMBER: US/09/257,825B
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: US 08/655,352
PRIOR FILING DATE: 1996-05-23
PRIOR APPLICATION NUMBER: US 60/014,743
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 1776
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-257-825B-10

Query Match 2.8%; Score 36.8; DB 4; Length 1776;
Best Local Similarity 56.7%; Pred. No. 0.11;
Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
OY 1074 TTATGGGAAGGTGATTTTGATGAACGCCAGAAATATCATATGCGGATGCGATGGAAC 1133
DB 1703 TTAATTTAAAGGATCTTTTACGAGTAGATATAAATATGATGATGAGAA 1644
OY 1134 GGTGAAGTGGTGGCTTGGCGCTTCATCATGTAAGAAAGGAGAAATCAATA 1193
DB 1643 GTTAGAGATATTAAATGAAATAGCGTGTATTCAAAATTAAGAGCAAAATTCATA 1584

RESULT 7
5231168-1
Patent No. 5231168
APPLICANT: DIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SOREN;
VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE H.
TITLE OF INVENTION: MALARIA ANTIGEN
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658

FILING DATE: 18-SEP-1989
SEQ ID NO: 1
LENGTH: 3095
5231168-1

Query Match 2.5%; Score 33.8; DB 6; Length 3095;
Best Local Similarity 48.7%; Pred. No. 1.5;
Matches 92; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
OY 1082 AAGGTGATTTGATGAACGCCAGAAATATCATATGCGGATGCGTGAACGATGACT 1141
DB 1199 AACATGAATAGTAGAGTGAAGAAATTTCTACAGAGATATAAATGAAAAGGTCAAC 1258
OY 1142 TGGTGAAGTGGCTTGGCGCTTCATCATGTAAGAAAGGAGCAAAATCAATCAATGAAG 1201
DB 1259 ATGAATAGTAGAGTGAAGAAATTTCTACAGAGATATAAATGAAAAGGTGAAC 1318
OY 1202 TGGTGAAGTGGCTTGGCGCTTCATCATGTAAGAAAGGAGCAAAATCAATCAATGAAG 1261
DB 1319 ATGAATAGTAGAGTGAAGAAATTTCTACAGAGATATAAATGAAAAGGTCAACATG 1378
OY 1262 AATAGTAG 1270
DB 1379 AATAGTAG 1387

RESULT 8
US-09-134-001C-982
Sequence 982, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 982
LENGTH: 981
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-982

Query Match 2.5%; Score 33.4; DB 4; Length 981;
Best Local Similarity 51.0%; Pred. No. 0.98;
Matches 79; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
OY 390 TCTCATATCATCTCTCGTCAACATATACCGGATATAGGACCCCTGTGATTC 449
DB 291 TTTTAACCTTATCTCGGATTAACATATATCTCCATATATGAAGAGTAGACCA 350
OY 450 ATTACAAAAGCTTGGCTAGCGTGAAGTGAAGACCTGTTGGAGCCCTTATGACTTAG 509
DB 351 AATGATATATGATGAATTAAGAAAGGAGTAACTGTTCTGCGCTCATATTATAG 410
OY 510 ATATGCTAGCTGCTGAAGGTACACCTTCACAG 544
DB 411 TTTTCTGTGCTCTTATGATCAACGTCGTCAG 445

RESULT 9
US-09-221-017B-881
Sequence 881, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 881:
SEQUENCE CHARACTERISTICS:
LENGTH: 2402 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...2402
US-09-221-017B-881

Query Match          2.4%: Score 32.6; DB 4; Length 2402:
Best Local Similarity 51.0%; Pred. No.3.1; Mismatches 74; Indels 0; Gaps 0.
Matches 77; Conservative 0;

QY 857 ACCCAAAATTTTGGTCCTCAAAAACCAATGATGTAAGTCCAAATTAGGCCTTATCG 916
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 662 ATGTGAATATCATGTTAATTCGCCGAGCAGAGACTGACCATTTTTGCTTTGCTTGG 721
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 917 CTCATGACATGCTGTTATTTTCTAAAAACATTTGTTTTCTCGAAGGGGTTATVCTTATG 976
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 722 TTGGTGCCACGATCGTTGTTGTGTGTCATAATGCTTATTCGCCACAGCGCTTATGGAG 781
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 977 AAACGAAATCTACCTTGATAGGAGACAT 1007
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 782 ATACGGAAGTCTACATTGGAGGAATCAT 812
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
US-08-206-176-1
Sequence 1, Application US/08206176
Patent No. 5639940
```

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GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Dallymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5943 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Human Fibrinogen A-alpha chain
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..84, 1154..1279, 1739..1922, 3055..3200,
3786..5210)
US-08-206-176-1
Query Match 2.4%: Score 32.4; DB 1; Length 5943;
Best Local Similarity 48.4%; Pred No.6.2;
Matches 90; Conservative 0; Mismatches 96; Indels 0; Gaps 0.
QY 861 AAAATTTTGGTCTCAAAAACCAATAGTGTACTCCATTTAGGCTTATTACGCTCA 920
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2657 AAATATTTGAATGCAATCAACCAACTATTTTAACTCCAAATTCACCTTTAAATTC 2716
QY 921 TGACATGCTGATATTTCTPAAAGACATTTGGTTTCCCTGAAGGGTTTATCTTAAGAAC 980
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2717 AAAGAAAGTCTCTCTATATTTCTTTGGGATTAATTTCTATAGACATCTTAAC 2776
QY 981 ACGATTTCTACCTTGATAGGAGCAATATAAACACACCAAGAGCGCTATTAATGATTAT 1040
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2777 TGGCATTTGAGGAAGGCTGCAGGCAATTAATTCACAAAGTCCCATAGGTT 2836
QY 1041 GGAAC 1046
|||
Db 2837 TTGAAC 2842
-
RESULT 11
US-08-687-865A-1
; Sequence 1, Application US/08687865A
; Patent No. 5855596
; GENERAL INFORMATION:
; APPLICANT: Jones, Kevin F.

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? APPLICANT: Zagursky, Robert J.
? APPLICANT: OOI, Peggy
? TITLE OF INVENTION: The Nuca Protein of Haemophilus
? TITLE OF INVENTION: Influenzae and the Gene Encoding That Protein
? NUMBER OF SEQUENCES: 23
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: American Cyanamid Company
? STREET: One Cyanamid Plaza
? CITY: Wayne
? STATE: New Jersey
? COUNTRY: U.S.A.
? ZIP: 07470
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/687,865A
? FILING DATE: 26-JUL-1996
? CLASSIFICATION: 536
? ATTORNEY/AGENT INFORMATION:
? NAME: Gordon, Alan M.
? REGISTRATION NUMBER: 30,637
? REFERENCE/DOCKET NUMBER: 33,250-00
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-831-3244
? TELEFAX: 201-831-3305
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2263 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 229..2037
? US-08-687-865A-1

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Query Match          2.4%: Score 31.6; DB 2; Length 2263;
Best Local Similarity 50.7%; Pred. No. 6.3;
Matches 76: Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1067 CATTGTTTATGGAAGCGTATTTGATGAGCGCCAGAAATATCATGCGGATGCG 1126
    ||| ||||| ||| | ||||| | ||||| ||| ||| ||| |||
DB 1694 CATTCCCTTATGTCGAGGTATTCGTATGAGCGCAATGAAACCAATGCGGAAGTA 1753

QY 1127 ATGGAACGCTGAACCTTGTCGACCTTGGCGCTTCAATCACTATGGAAGAAGAGAAA 1186
    | | |||| | |||| | |||| | |||| | |||| | ||||
DB 1754 ACCGTTTACTGAGTGTGGAAGTCTTGAAATAAACCAACCAACATGGAACGATTGATG 1813

QY 1187 ATCAATACCTTAAGCTGTTAGATGATG 1216
    ||| | ||| | ||| | ||| | ||| | ||| | |||
DB 1814 ATACAAACGTTATCTTGTGGAACAATG 1843

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RESULT 12
US-09-043-711-1
; Sequence 1, Application US/09043711
; Patent No. 6221365
; GENERAL INFORMATION:
; APPLICANT: Jones, Kevin F.
; APPLICANT: Zagursky, Robert J.
; APPLICANT: OOI, Peggy
; TITLE OF INVENTION: The Nuca Protein of Haemophilus
; TITLE OF INVENTION: Influenzae and the Gene Encoding That Protein
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey

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? COUNTRY: U.S.A.
? ZIP: 07470
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/043,711
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/687,865
? FILING DATE: 26-JUL-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Gordon, Alan M.
? REGISTRATION NUMBER: 30,637
? REFERENCE/DOCKET NUMBER: 33,250-00
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-831-3244
? TELEFAX: 201-831-3305
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2263 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 229..2037
? US-09-043-711-1

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```

Query Match          2.4%: Score 31.6; DB 4; Length 2263;
Best Local Similarity 50.7%; Pred. No. 6.3;
Matches 76: Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1067 CATTGTTTATGGAAGCGTATTTGATGAGCGCCAGAAATATCATGCGGATGCG 1126
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DB 1694 CATTCCCTTATGTCGAGGTATTCGTATGAGCGCAATGAAACCAATGCGGAAGTA 1753

QY 1127 ATGGAACGCTGAACCTTGTCGACCTTGGCGCTTCAATCACTATGGAAGAAGAGAAA 1186
    | | |||| | |||| | |||| | |||| | |||| | ||||
DB 1754 ACCGTTTACTGAGTGTGGAAGTCTTGAAATAAACCAACCAACATGGAACGATTGATG 1813

QY 1187 ATCAATACCTTAAGCTGTTAGATGATG 1216
    ||| | ||| | ||| | ||| | ||| | ||| | |||
DB 1814 ATACAAACGTTATCTTGTGGAACAATG 1843

```

```

RESULT 13
US-09-146-053-4
; Sequence 4, Application US/09146053A
; Patent No. 639349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Jerry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Amino-peptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-4

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Query Match 2.4%: Score 31.6; DB 4; Length 50000;

```

CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-289-653-1

Query Match
Best Local Similarity 57.7%: Pred. No. 8.4;
Matches 56; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 405 TCGTCTCAAGATATACCCGGATACATGCGACCCCTGGTAGATTGATTAACAAGAAGCTTG 464
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2650 TCGCATTCACAGCACACCATRACCATTGTGCCCTTGCGAGCTGCAGTCACAACTAAGT 2591

QY 465 CTACGCTGATGGTGAGACTGTGTTGGAAGCCCTTAT 501
      || |||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2590 CTCGCGCTCCTGTCAAGGCTGTGTTGAACCAACAAT 2554

RESULT 15
US-09-484-970B-106/C
Sequence 106, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 106
LENGTH: 4822
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
NAME/KEY: unsure
LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809
OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106

Query Match
Best Local Similarity 53.7%: Score 31.4; DB 4; Length 4822;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 157 AGGTGACCATTACATAAGCCCTCTACTTCATCTCGAATCATGGTACCCCTTCATC 216
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Db 2312 AGCTGCATTATATTTTCAGGCTCTTATATTTCTTCCTTTATTCCTGATCACTTTTTAG 2253

QY 217 AAGAAAAGATGCATGGTTCAGACTTGGTTGATTCCAGTGCATCTGCTCTTC 276
      | | || || || || || || || || || || || || || || || || || || || ||

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Db 2252 TGATGACCTCATGCGCTCTTCATATGCGGGGCTTTCAGGCTCATGTTTATGCTTC 2193
Qy 277 A 277
Db 2192 A 2192

Search completed: February 15, 2003, 13:16:59
Job time : 116 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:58:02 : Search time 66 Seconds
(Without alignments)
10279.077 Million cell updates/sec

Title: US-09-857-612A-13
Perfect score: 1332
Sequence: 1 atgaagaagaacaaga.....gtaattgttcggggttaa 1332

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 42439 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_NA:*

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2: /cgn2_6/pdata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/pdata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/pdata/1/pubpna/US07_NEW_PUB.seq:*
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14: /cgn2_6/pdata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	436.6	32.8	1242	9	US-09-938-842A-376
2	155.6	11.7	1048	9	US-09-998-059-8
3	155.6	11.7	1059	9	US-09-998-059-20
4	155.6	11.7	1080	9	US-09-998-059-27
5	64.6	4.8	1744	10	US-09-919-497-30
6	64.6	4.8	1744	10	US-09-880-107-2245
7	60.4	4.5	2680	9	US-09-978-295A-156
8	60.4	4.5	2680	9	US-09-978-697-156
9	60.4	4.5	2680	9	US-09-978-192A-156
10	60.4	4.5	2680	9	US-09-999-832A-156
11	60.4	4.5	2680	9	US-09-978-189-156
12	55.4	4.2	248	10	US-09-923-876-2515
13	51.2	3.8	2180	9	US-10-001-054-7
14	36	2.7	954	10	US-09-947-971-3
15	36	2.7	640681	10	US-09-790-988-1
16	34.2	2.6	312	10	US-09-880-107-3898
17	34.2	2.6	2364	12	US-10-044-090-37
18	34.2	2.6	32199	10	US-09-764-855-210
19	33.8	2.5	239	10	US-09-983-965-5347

20	33.6	2.5	1154	10	US-09-867-550-1491	Sequence 1491, Ap
21	33.4	2.5	878	9	US-09-828-995B-57	Sequence 57, Appl
22	33.4	2.5	878	9	US-09-828-995B-59	Sequence 59, Appl
23	33.4	2.5	1095	9	US-09-828-995B-65	Sequence 65, Appl
24	33.4	2.5	1095	9	US-09-828-995B-67	Sequence 67, Appl
25	33.4	2.5	1158	9	US-09-828-995B-63	Sequence 63, Appl
26	33.4	2.5	1158	9	US-09-828-995B-64	Sequence 64, Appl
27	33.4	2.5	1454	9	US-09-828-995B-60	Sequence 60, Appl
28	33.4	2.5	1454	9	US-09-828-995B-62	Sequence 62, Appl
29	33.2	2.5	1722	10	US-09-823-101-3	Sequence 62, Appl
30	33.2	2.5	1698	10	US-09-815-742-7160	Sequence 7160, Ap
31	33	2.5	1998	10	US-09-833-381-1139	Sequence 1139, Ap
32	32.6	2.4	2769	10	US-09-739-254-53	Sequence 53, Appl
33	32.6	2.4	2769	10	US-09-964-615-53	Sequence 53, Appl
34	32.6	2.4	3849	10	US-09-764-864-560	Sequence 560, Ap
35	32.6	2.4	3850	10	US-09-764-864-113	Sequence 113, Ap
36	32.6	2.4	6819	9	US-10-098-841-4	Sequence 4, Appl
37	32.2	2.4	484	9	US-10-046-935-620	Sequence 620, Ap
38	32.2	2.4	484	9	US-09-878-178-620	Sequence 620, Ap
39	32.2	2.4	1412	10	US-09-925-301-568	Sequence 568, Ap
40	32.2	2.4	1969	10	US-09-729-674-7	Sequence 7, Appl
41	32	2.4	267	10	US-09-923-876-4976	Sequence 4976, Ap
42	32	2.4	2082	9	US-09-893-519A-105	Sequence 105, Ap
43	32	2.4	6114	9	US-09-938-842A-2700	Sequence 2700, Ap
44	32	2.4	66804	10	US-09-740-041-3	Sequence 3, Appl
45	31.8	2.4	765	10	US-09-897-214-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-938-842A-376
Sequence 376, Application US/09938842A
Patent No. US0020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRI300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300, 111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 376
LENGTH: 1242
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-376
Query Match 32.8%; Score 436.6; DB 9; Length 1242;
Best Local Similarity 62.3%; Pred. No. 1.3e-119;
Matches 767; Conservative 0; Mismatches 434; Indels 30; Gaps 4;
OY 74 TGTCTTCTTCTATGCATGTGGGCGACACCTTGTGATTTAATACAGTA 133
DB 2 TGACCTCATGTGTCACCTGTGGGTACACAGTCTTGTGATTTGTCAGGAA 61
OY 134 ACGGAGGACCAATACAGAGGTGACCAATCAGTACAGCCCTTACTTCACT 193
DB 62 ACGGAGGATACAGTATACAGTACGCTGACAGATTAAGCAAGTGTCTGCT 121
OY 194 GCGAATCATGTACCTCTCATCAAGAAAGA--ATGATGTGTTCAGACTTGGTTG 250
DB 122 GTAGACGTGTTATATCCGATTATAGAGAGTGTGATGTTAGGCTATGCTTG 181

[illegible]

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RESULT 6
US-09-880-107-2245
: Sequence 2245, Application US/09880107
: Patent No. US20020142981A1
: GENERAL INFORMATION:
: APPLICANT: Horne, Darci T.
: APPLICANT: Vockley, Joseph G.
: APPLICANT: Scherf, Uwe
: APPLICANT: Gene Logic, Inc.
: TITLE OR INVENTION: Gene Expression Profiles In Liver Cancer
: FILE REFERENCE: 44921-5028-WO
: CURRENT APPLICATION NUMBER: US/09/880,107
: CURRENT FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/237,054
: PRIOR FILING DATE: 2000-10-02
: NUMBER OF SEQ ID NOS: 3950
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2245
: LENGTH: 1744
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020142981A1 MI2625
US-09-880-107-2245

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Oy	220	AAAAAGATGATGGTTGCTCAGACTTTGGTTGGTTTGCATTCCAGTGTCTACTCTGCTCTTTCACT				279
Db	496	AAGACAGAGGACTTTCCTCACCATCTGGCTGGATTCACACATGTTCTTACCCCTTGGGGTAA				555
Oy	280	CATAGCTTTGGCGAAGCCGATGACCCCTTCATTACACCAAGAAGCTCGATGATTACTTTCACAC				339
Db	556	GAGTCGTGATTCGATATACACCAGGGTTTGTCTACACACCGAGTCTGGGCTGCTGTCCAAC				615
Oy	340	ACTCTGTGGGTTGAGACCCGGTCCCTCATTCTTTGGTTCCACCACACTCTCTTCTATCTC				399
Db	616	GCCCCTGTGTTCAGGATCCGGCTCCCTGGCTTTGGCAAGACTACTCTGTGGAGTACCG				675
Oy	400	AATCCTCTCTCAAGCATATCACGGAATACATGCGACCCCTGTGATTCATTATCAAAAG				459
Db	676	GACAG-----CAGAACCTGGCAGGGTACCTGCACACACTGTGTCAAGAACTGGTCAC				729
Oy	460	CTTGGCTACGCTGATGTGTGAGACTCTGTTTGGAGCCCTTATGACTTTAAGATATGGTCTA				519
Db	730	AATGCTACATCGTGGCGGAGACACTGTGGCGCGCCCTTATGACTG-----				776

QY	520	GGGCTGAAGGTACACCTTGTACAAAGTGGGTCCAACTTCTTCAAGATCTAAGAAATTGG	579
Db	777	GGGGCTGAAGCCCGGGCCAGGAGAGGT-----ACTACCCGAAAGCTGCAGGGCTGGT	830
QY	580	ATTAAAGAACCAAGCAATTTCCAAATAATGGGAAGCCAGTATACCTTCTCCACAGTTTA	639
Db	831	GGAGGAAATGACAGS-----CTGGCTATGGGAAGCCGTGTCTTCTCATTTGGCCACAGCCTC	885
QY	640	GGAGGCGTATTTGTCTCAACACTACTAAATAGAAACCCGCCCTTGGCGCAAAAAATTTC	699
Db	886	GGCTGTCTCAACTGTCTCTATTCTTCGTGCGCCAGACCCGACGGCTGGAAAGGACCGCTTT	945
QY	700	ATCAACACTTTCATTTGCTCTTTCAGCTCCATGAGGGGTGTCATATAGACGAATGTACACC	759
Db	946	ATTGATGGCTTCAATCTCTCTTGGGGCTCCCTCGGGGTGGCTCCATCAAGCCATGCTGGTC	1005
QY	760	TTTTCATCTGCGCAACACTTTTGGGAGTGGCCCTTAGTGGACCCTTTATATAGTGGAGATGAA	819
Db	1006	TTTGGCCCTCAGGTAGACAACCAAGGCGATCCCCATCATCTTCAGCATCAAGCTGAAGAGAGAG	1065
QY	820	CAAGAAGAGTCTCGAGAGTAACTTTTGGCTTTTGGC	854
Db	1066	CAGCGCATTAACCAACACACTCCCTCTGGATGTTTCC	1100

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: RESULT 7
: US-09-978-295A-156
: Sequence 156, Application US/09978295A
: Patent No. US20020156006A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Baton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J
: APPLICANT: Kiljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Peoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC11
: CURRENT APPLICATION NUMBER: US/09/978,295A
: PRIOR FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066364
: PRIOR FILING DATE: 1997-11-21
: PRIOR APPLICATION NUMBER: 60/077450

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[illegible]

; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 4.5% Score 60.4; DB 9; Length 2680;
 Best Local Similarity 44.3% Pred No. 1.3e-07;
 Matches 418; Conservative 0; Mismatches 496; Indels 30; Gaps 3;

QY 205 TACCTCTCATAGAAAAGATGGATGGTTCAGACTTTGGATTGATTCAGTGTCAATA 264
 DB 207 TACCTCTCTCAAGAAAGACCAAGACTTACAAATCGGTGTAAGTGAAGTGTG 266
 QY 265 CTTCCTCTTTCACATATGCTTTGCCGAACGATGACCTTTCATTACCAACAAGACTG 324
 DB 267 CTTCCTCTTTCACATATGCTTTGCCGAACGATGACCTTTCATTACCAACAAGACTG 326
 QY 325 GATGATTAATCTCAACACTCTCGGGTGGAGACCGGGTCCCTCACTTTGGTCCACCAAC 384
 DB 327 AGGGCCACCCACTTTCCTATGATGTGTGATGATGATGATGATGATGATGATGATGATG 386
 QY 385 TCTCTTCTATCTCAATCTCTGTCAGAGATATCACCGGATACAGGATGACACCCCTGTGA 444
 DB 387 TCACGTGAGTCTCTGAGACCCCAAGAAAGACGCTGGGTTCTATTTCCACACATGATG 446
 QY 445 GATTCATTACAAAAGCTTGGCTACGCTGATGTGAGACTCTGTGGAGACCCCTTATGAC 504
 DB 447 GAGACCCCTTGTGGCTGAGGCTACACACGCGGTGAGGATGTCGAGGCGCTCCCTCATGAC 506
 QY 505 TTTAGATATAGTCTAGCTGCTGAGGTCAACCTTCAAGTGGTTCAGATTTCTCAAA 564
 DB 507 TGGCCCGACGCCCCAATATGAAAAGCGGCCCTTCTGCGCCCTCCGGAAGTATGATGAG 566
 QY 565 GATCTAAAGATTTGATGATGAGAGACAGCAATTCATATGGAAGCCAGTATACTT 624
 DB 567 GAGATGTACACAGCTCT-----ATGGGGGCGCCCTGGTGCTG 602
 QY 625 CTTCGCCACAGTTTAGAGGCGCTATTTGCTTCAACTACTAATAATGAAGCCCGCTTCT 684
 DB 603 GTTGCCTCAGATGTGGAACATGTACAGCTTCTACTTCTGACCGGAGCGGAGCGGC 662
 QY 685 TGGCCCAAAAATTCATCAAAACACTTTCATTTGCTTTCAGTCCATGAGGCTGTCTATA 744
 DB 663 TGGAGGACAATATATCCGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
 QY 745 GACGAATGTACACTTTGCTGCTGCAACACTTTGGGAGTGCCTTATGATGACCTTTA 804
 DB 723 AAGACCTCTGCGGCTCTGCTGCTGCAAGACAACCGGATCCAGTATCGGGCCCTG 782
 QY 805 TTAGAGAGGATGAGCAAAAGAGCTCCGAGATACCTTTGGCTTTTGGCTTATACCCAAA 864
 DB 783 AAGATCCCGGAGACAGCGGTCACTCTCTCCACACCTGCTCTCCCTCAACATAC 842
 QY 865 ATTTTGTCTCTCAAAAACCAATAGTATGATTAAGCTTCAATTAAGCTTTCAGACTCATGAC 924
 DB 843 AACTGTCTCACTGACAAAGTGTGTGCAAGACACCAATCACTAATCACTGCGGAGC 902
 QY 925 ATGTTGATTTTCTTAAAGACATGGTTTTTCTGGAAGGGGTTTATCTTATGAACACAGA 984
 DB 903 TACCGCAAGTTCTTCCAGACATCGGCTT---TGAAGATGGCTGCTCATGCGGAGAGAC 959
 QY 985 ATTCTACCTTGTATGAGGAACATTAAGACACCAAGTCCCTATATACCTTATATATGGA 1044
 DB 960 ACAGAAAGGCTGTGTGAAGCAAGTGCACCTGCGAGCTGACAGCTGCTCTATGAT 1019
 QY 1045 ACGGAGTGTGGAACCTTGGAAACATGTTTATGGAAGAGGATTTGATGATGAGCGGCA 1104
 DB 1020 ACTGGCGTCCCAACACAGACTCTTCTTACTATGAGA--GCTTCCCTGAGCGTGAACCT 1076

QY 1105 GAATATCATATGGAGTGTGATGGAACGCTGTAAGCTTGTGAG 1148
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RESULT 8
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 ; Sequence 156, Application US/09978697
 ; Patent No. US20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gertsen, Mary E.
 ; APPLICANT: Godowski, Audrey
 ; APPLICANT: Grimaldi, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C27
 ; CURRENT APPLICATION NUMBER: US/09/978,697
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/085704
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 4.5%; Score 60.4; DB 9; Length 2680;
Best Local Similarity 44.3%; Pred. No. 1.3e-07;
Matches 418; Conservative 0; Mismatches 496; Indels 30; Gaps 3;

QY 205 TACCTTCATCAAGAAAAGATGATGTTGACAGCTTTGTTGATTCAGTCTCAT 264
DB 207 TACCTTCATCAAGAAAAGATGATGTTGACAGCTTTGTTGATTCAGTCTCAT 266
QY 265 CTTCCTCTTTCATCATGCTTTGCGGACGACGACCTTCATTACACCAAAACTC 324
DB 267 CTTCCTCTTTCATCATGCTTTGCGGACGACGACCTTCATTACACCAAAACTC 326

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PRIOR APPLICATION NUMBER:	60/080155
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26	PRIOR FILING DATE: 1998-05-13
27	PRIOR APPLICATION NUMBER: 60/085582
28	PRIOR FILING DATE: 1998-05-15
29	PRIOR APPLICATION NUMBER: 60/085700
30	PRIOR FILING DATE: 1998-05-15
31	PRIOR APPLICATION NUMBER: 60/085688
32	PRIOR FILING DATE: 1998-05-15
33	PRIOR APPLICATION NUMBER: 60/085579
34	PRIOR FILING DATE: 1998-05-15
35	PRIOR APPLICATION NUMBER: 60/085580
36	PRIOR FILING DATE: 1998-05-15
37	PRIOR APPLICATION NUMBER: 60/085577
38	PRIOR FILING DATE: 1998-05-15
39	PRIOR APPLICATION NUMBER: 60/085704
40	PRIOR FILING DATE: 1998-05-15
41	PRIOR APPLICATION NUMBER: 60/085697
42	PRIOR FILING DATE: 1998-05-15

Query Match	4.5%;	Score 60.4;	DB 9;	Length 2680;
Best Local Similarity	44.3%;	Pred. No. 1.3e-07;		
Matches 418; Conservative	0;	Mismatches 496;	Indels 30;	Gaps 3;

OY	205	TACCCCTGCATCAAGAAAAGAAATAGATAGTGTCTGCAGCTTGTGGTATTCAGATGTATA	264
	206		
Db	207	TACTCTCTCTCCAGAGAGACCGAAAGCTACTTTCACATCTGGCTGAACCTGGAACTGCTG	266
OY	265	CTTGCTCCCTTTCACCAATGCTTTGGCCGAGACGATGACCCCTTCATTTCACACAGAAGATC	324
Db	267	CTGCCTGTCATCATTTAGACTGCTGGATTGACAAATTCAGAGCGTGGTTTACACAAAACATTC	326
OY	325	GATGATTACTTCACACTCTCTGGGGTTGAGACCCGGGTCCCTCACTTTGGTTCACCAAC	384
Db	327	AGGGCACCCAGTTTCCATGATGTGTGGATGTAGCTGTCCCTGGCTTTGGGAGAACCTTC	386
OY	385	TCTCTCTCTATCTCAATCTCTGTCTCTCAAGATATTCACCGGATATTCATGAGACCCCTGTGA	444
Db	387	TCACGTGAGATCTCTGACACCCAGCAAAAGACGCGGGTTCCTATTTCCACACCATGTG	446
OY	445	GATTCATTACAAAAGCTTGGCTACGCTATGTGATGAGACTCTGTTTGGAGCCCTTATGAC	504
Db	447	GAGAGCCTTGTGGGGCTGTGGGGCTACACACGGGGTGAAGATGTGCCAGGGGCTCCCTATGAC	506
OY	505	TTTAGATATGCTCTAGCTGCTGAAGGTCACCCCTTCACAGTGGGTTCCAAAGTTCTCAAA	564
Db	507	TGGCCCGAGCCCAATAATGAAAAGGGGGCTTACTTCTCGGCCCTCGCCGAGATGATGAG	566
OY	565	GATCTAAAGAAATTTGATAGAAAGAAACAGCAATTCATTAATGGGAAGCCAGTATACTT	624
Db	567	GAGATGTACCAAGCTT-----ATGGGAGGCCCGGTGGTCTG	602

CURRENT APPLICATION NUMBER:	US-02/99,832,200
PRIOR FILING DATE:	2001-10-24
PRIOR APPLICATION NUMBER:	09/918585
PRIOR FILING DATE:	2001-07-30
PRIOR APPLICATION NUMBER:	60/062250
PRIOR FILING DATE:	1997-10-17
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PRIOR APPLICATION NUMBER:	60/065311
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PRIOR APPLICATION NUMBER:	60/066364
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PRIOR FILING DATE:	1998-03-25
PRIOR APPLICATION NUMBER:	60/079636
PRIOR FILING DATE:	1998-03-26

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PRIOR APPLICATION NUMBER: 60/077779	PRIOR FILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: 60/078888	PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE:	1998-04-29
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PRIOR FILING DATE:	1998-05-07
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PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084643
PRIOR FILING DATE:	1998-05-07

Query Match	4.5%;	Score 60.4;	DB 9;	Length 2680;
Best Local Similarity	-44.3%;	Pred. No. 1.3e-07;		
Matches 418; Conservative	0;	Mismatches 496;	Indels 30;	Gaps 3;

OY	205	TACCTCTCATCAAGAAAAGAAATGAGATGGTTCAGACTTTGGTTGATTCACGATCATATA	264
Db	207	TACCTCTCTCCAAAGAAAGACCGAAAGCTACTTTCACAACTGTGGCTGMACTGGAACTCTG	266
OY	265	CTTGCCTCTTCTCACTCAATGCTTTTCCGGAACGATGACCCCTTCAATTAACCAAGAAATC	324
Db	267	CTGCCTGTCACTCAATTAATGACTCTGGATTTGCAATTTCAAGGGCTGTGGTTTCAACAAACATTC	326
OY	325	GATGATTTACTTCAACACTCCCTGGGGTTGAGACCCGGGGCCCTCACTTTGGTTGGACCAAC	384
Db	327	AGGGCCACCCAGTTTCTTGATGTGTGATATACGTGTCTCTGGCTTTTGGGAAGACTTC	386
OY	385	TCCTCTCTATCTCAATTCCTCGTCTCAAGCATATCAACCGGATACATGGACCCCTGGTA	444
Db	387	TCACGTGAGTTCTTGAGACCCGAGAAAGACGCTGGGTTCTATTTCACACATATGGTG	446
OY	445	GATTCATTAACAAGAAAGCTTGGCTAGCGCTGATGTGTAGACTCTGTTTGGAGCCCTTAAGAC	504
Db	447	GAGAGCCCTTGTGGGCTGGGGCTGTACACACGGGTGAGATGTGCCAGGGGGCTCCCTATGAC	506
OY	505	TTTAGATATGTGCTAGCTAGCTGAGAGGTACCCCTTCAACAATGGGTTTCCAAATTTCTTAAA	564
Db	507	TGGGGCCGAGGCCCAATATGAAGAAAGGGGCCCTACTTCTGTGGGCCCTCCGAGATATGTGAG	566
OY	565	GATCTAAAGAAATTGTATATGAAGAAAGCAACATTCAAATATGGGAAGCCAGTATACTT	624
Db	567	GAGATGTATCCGAGCTGT-----ATGGGGGGCCCGCTGGTGGCTG	626
OY	625	CTCTCCCACTGTTTGAAGAGGCGCTATTTGTCTTACAACTACTTAATATAGAAACCCGCCCT	684
Db	603	GTTGCCCACTGATATGGGCAACATGTACACGCTTCACTTTTGTGCAAGGGCAAGCCGACAGCC	666
OY	685	TGGCGCAAAAAATTCATCAAAACACTTCATTTGCTTTTCAGCTTCATGGGGTGTGTATATA	744
Db	683	TGGAAGGACAGATATATCCGGGGCTTCGTGTCACTGTGGGTGGCCCTGGGGGGGGTGGTGGC	722
OY	745	GACCAAAATGTACACTTGTGCATCTGGGCAACACTTTGGGAGTGGCCCTAGTGTGACCCCTTAA	804
Db	723	AAGACCCCTGGCGCTCTGGCTTCAAGGAGACAACAACCGGATCCCAATGTCATGCGGCGCCCTG	782
OY	805	TTTAGTGAAGGATGGAACAAGAAGCTCCGAGAGTAACTTTGGCTTTTGGCTTAACCCAAAA	864
Db	783	AAGATCCGGGAGCAGACAGCGGTCAAGCTGTCTCCACACAGCTGGCTGTGCTTACAACTAC	842
OY	865	ATTTTGTGCTCAAAAAACCAATATGTATATACCTCAATTAAGCTTATTAAGCTCATGAC	924
Db	843	ACATGTGCTACCTGGAAGAGTGTCTGTGAGACACCCCAATCAACACTACACATCTGGGGAG	902

Sequence 2515, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Laigudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ico)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 2515
LENGTH: 248
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700160724H1
US-09-923-876-2515

Query Match 4.2%; Score 55.4; DB 10; Length 248;
Best Local Similarity 54.7%; Pred. No. 1.1e-06;
Matches 110; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 423 CGGATACATGGCACCCTGTATATTCATTACAAAGCCTTGGCTGACGCTGATGTGAGAC 482
DB 26 CTGGTCCCTCGGAAGCTGAGCCCGCAGCAAGACATGGGATACCGAGACGAGACAC 85
QY 483 TCTGTTGAGCCCTTATGACTTTAGATGTTGCTAGCTGCTGAAGGTACCCCTTCACA 542
DB 86 CATGTTGGAGCCCTTACGACTTCGGCTAGCGCCGCTCCCGCGGCAAGACGTCGCA 145
QY 543 AGTGGCTTCCAGCTTCTCAAGATCTTAAAGATTTGATGAGAAGCAAGCAATTCCAA 602
DB 146 GGTGTACTCCGCTACTTCAGAGCTGATGAGCTGTGTCGAGCGCAGGAGAGAGAC 205
QY 603 TATGGGAAGCCAGTGACT 623
DB 206 CCGGAAGAGCGCTCATCT 226

RESULT 13
US-10-001-054-7
Sequence 7, Application US/10001054
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Hebert, Carolyn
APPLICANT: Henzel, William
APPLICANT: Kabakoff, Rhona
APPLICANT: Shelton, David
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
FILE REFERENCE: P3034RI.PCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 60/082999
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PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/096894
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QY	665 TAAATGAACACCCCTCTTGGCCAAAAAATTATCAACACTTCAATGTCTTTGCG	724		
DB	143 TGCAGCCGACACCGAGGCTCGAAGGACAACTATATCCGGCCCTTCCGTCACTGGGAG	202		
QY	725 CTCACATGGGGTGGTCTATAGACAAATGTACACCTTTCATCTGGCAACCTTTGGAG	784		
DB	203 CGCCCTGGGGGGGCGCTGGCCCAAGACCTGCGCTGCTTGGTACAGACCAACACCGGA	262		
QY	785 TGCCCCATAGTGAGACCTTATATAGTAGAGGATGAACAAGAAAGCTCCGAGATTAACCTTT	844		
DB	263 TCCAGTATATGGGGCCCTGAAGATCCGGGACACAGCGGTGTCAGTGTCTCCACAGCT	322		
QY	845 GGCCTTTGCTTAACCCAAAAATTTTGGTCTCTCAAAAAACCAATAGTATACTCCAAATTA	904		
DB	323 GCGCTGCTCCCTACACTACACATGTGTACCTGAAAGAGTGTCTGCGACACCCACAA	382		
QY	905 GGCCTTATTCAGTCATACATGTTGATTTTCTAAAGACATTTGGTTTTCTCGAAGGGG	964		
DB	383 TCACACTACACACTGGGAGCATPCGCCAGATTTCTCCAGAGCAATCGGCTT--TGAAGATG	439		
QY	965 TTTATCTTATGAACAACGAATTTACCCCTTGATAGGAAACATTAAGACCCACAAGTGC	1024		
DB	440 GCTGGCTCATCGGAGGACACAGAAGGGCTGTGTGGAAAGCCACGATGCCAGTGGGGTGC	499		
QY	1025 CTATTACTTGTATTAATGAGGAACGGAGTGGGAACCTTGGAAAAATTTGTTTATGGGAAG	1084		
DB	500 AGCTGCACACTGCTCTATGTGACTGGCGTCCACACACAGACTCTTCTACTATGAGAGCT	559		
QY	1085 GTGATTTGATGAACGGCCACAAATATCATATGGGAGATTCGTATGGAACGGGAACCTGG	1144		
DB	560 TCCCTGCACCGTAC--CTTAAATCTCTTGGTGGACGGCCGATGTACTGTACACTTGA	616		
QY	1145 TGAG 1148			
DB	617 AGAG 620			

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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 11:56:47 : Search time 1677 Seconds
(without alignments)
12863.678 Million cell updates/sec

Title: US-09-857-612a-13
Perfect score: 1332
Sequence: 1 atgaagaagaagaagaaga.....gtattgtttcggggtaa 1332

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estda:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
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26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524.6	39.4	532	13	B1973838 sa193d08.
2	515.8	38.7	527	10	AM759200 s138c06.Y
3	432	32.4	507	14	BM885973 sam10d11.
4	333.8	25.1	650	12	BG524903 8-8 Stev1
5	322.6	24.2	673	10	BE322181 NF010H121
6	305.8	23.0	648	14	BQ852109 QCB17C13.

Result No.	Score	Query Match	Length	DB ID	Description
7	296.2	22.2	630	14	BQ855578 QCB27B05.
8	256.6	19.3	587	12	BG523648 34-12 Ste
9	235	17.6	596	12	BG525847 54-55 Ste
10	234.6	17.6	635	12	BG522086 18-18 Ste
11	216.8	16.3	616	12	BG526525 60-13 Ste
12	205.2	15.4	527	14	BQ864610 QGC27C22.
13	195.4	14.7	618	10	AV441327 AV441327
14	171.6	12.9	600	10	AV827187 AV827187
15	170.8	12.8	529	10	AV442635 AV442635
16	166.8	12.5	724	12	BG127829 BG127829
17	153	11.5	514	10	AV528103 AV528103
18	146.6	11.0	537	12	BE355801 BE355801
19	143.8	10.8	163	13	BE801241 sr11d10.Y
20	143.4	10.8	676	17	BH578169 BH578169
21	134.8	10.1	401	13	B1139236 B1139236
22	122.6	9.2	517	13	B1209019 B1209019
23	122.6	9.2	517	13	B1209572 B1209572
24	122.6	9.2	517	13	B1210034 B1210034
25	122.6	9.2	517	13	B1210853 B1210853
26	117.4	8.8	657	13	B1256228 B1256228
27	116.6	8.8	593	17	BH777228 BH777228
28	115.4	8.7	416	13	BT069567 BT069567
29	114.8	8.6	419	10	AV816862 AV816862
30	114.8	8.6	731	13	B1406095 B1406095
31	100.4	7.5	430	10	AV797479 AV797479
32	91.8	6.9	673	13	B1261764 B1261764
33	86.8	6.5	637	14	BQ459510 BQ459510
34	85.8	6.4	323	14	BQ862413 BQ862413
35	84.4	6.3	518	12	BF557056 BF557056
36	79.6	6.0	1350	11	AK004914 AK004914
37	79.4	6.0	362	14	BQ984301 BQ984301
38	75.8	5.7	669	12	BG836492 BG836492
39	75.2	5.6	610	13	BM099858 BM099858
40	74.8	5.6	610	13	BM420443 BM420443
41	74	5.6	661	13	B1278186 B1278186
42	73	5.5	524	14	BQ243462 BQ243462
43	73	5.5	640	13	B1283237 B1283237
44	69.4	5.2	538	10	BE343728 BE343728
45	69	5.2	377	13	B1268541 B1268541

ALIGNMENTS

RESULT 1
B1973838
LOCUS
DEFINITION
sa193d08.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl065-8607 5' similar to TR:Q9ZM42 Q9ZM42 F17L21.28. ;, mRNA
Sequence.
ACCESSION
B1973838
VERSION
B1973838.1 GI:16348243
KEYWORDS
EST.
SOURCE
soybean.
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 532)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvelli,V., Khanna
'A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers
'Y., Peterson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
'R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
'R., Waterston,R. and Wilson,R.
Public-soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: cdueresgen.com
 High quality sequence stop: 421.

FEATURES

source

1..532
 Location/Qualifiers
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl065-8607"
 /clone_1lb="Gm-cl065"
 /tissue_type="germinating shoots"
 /lab_host="DH10B"
 /note="Vector: pBluescript II SK+; Site_1: EcoRI; site_2:
 xhoI; The cDNA library was constructed from mRNA isolated
 germinating shoots of the cultivar Williams. The seeds
 were allowed to germinate for 24 hours prior to being
 cold stressed for 2 days at 4C. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with a XhoI restriction site. EcoRI
 adapters were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA fragments were
 directionally cloned into the EcoRI-XhoI restriction site
 of the pBluescript vector. The ligated cDNA fragments were
 transformed into DH10B host cells (GibcoBRL). This library
 was constructed in the laboratory of Dr. Randy
 Shoemaker."

BASE COUNT 168 a 87 c 124 g 152 t 1 others
 ORIGIN

Query Match 39.4%; Score 524.6; DB 13; Length 532;
 Best Local Similarity 99.1%; Pred. NO. 3e-148;

Matches 527; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 759 CTTTCATCTGGCAGACACTTTGGAGTGGCCCTAGTGGACCTTTATTAGTAGGATGA 818
 |||||||
 Db 1 CTTTCATCTGGCAGACACTTTGGAGTGGCCCTAGTGGACCTTTATTAGTAGGATGA 60
 OY 819 ACAAGAAGCTCCGAGAGTAGTACCTTTGGCTTTGCCCTAACCCAAAATTTTGGTCCCA 878
 |||||||
 Db 61 ACAAGAAGCTCCGAGAGTAGTACCTTTGGCTTTGCCCTAACCCAAAATTTTGGTCCCA 120
 OY 879 AAACCAATAGTAGTACCTCAATTAGGCTTATTCAGCTCATGACATGTTGATTTCT 938
 |||||||
 Db 121 AAACCAATAGTAGTACCTCAATTAGGCTTATTCAGCTCATGACATGTTGATTTCT 180
 OY 999 AAACCAATAGTGGTTTCCCGAAGGGGTTTATCCTTATGAACACGAATTTCTACCTTGT 998
 |||||||
 Db 181 AAACCAATAGTGGTTTCCCGAAGGGGTTTATCCTTATGAACACGAATTTCTACCTTGT 240
 OY 999 AGGGAACATTAAGGACGACCAAGTCCCTATACCTTATTTATGGAACGGAGTGGGAC 1058
 |||||||
 Db 241 AGGGAACATTAAGGACGACCAAGTCCCTATACCTTATTTATGGAACGGAGTGGGAC 300
 OY 1059 CTTGGAACATTTGTTTATGGGAAAGGTGATTTGATGAACGGCCAGAAATATCATATGG 1118
 |||||||
 Db 301 CTTGGAACATTTGTTTATGGGAAAGGTGATTTGATGAACGGCCAGAAATATCATATGG 360
 OY 1119 GGATGGTATGGAACGGTCACTTGGTGAAGCTTTGGGCTTCAATCCTATGGAAGA 1178
 |||||||
 Db 361 GGATGGTATGGAACGGTCACTTGGTGAAGCTTTGGGCTTCAATCCTATGGAAGA 420
 OY 1179 GGAGAAAATCAATACCTTAAGGTGTTTAAATAGATGAGTGGGCTTCATACCTTCAAT 1238
 |||||||
 Db 421 GGAGAAAATCAATACCTTAAGGTGTTTAAATAGATGAGTGGGCTTCATACCTTCAAT 480
 OY 1239 TAAGATGATAGTGCATTAATGAATAGTAGTGAATTAATTAATTAAT 1290
 |||||||
 Db 481 TAAGATGATAGTGCATTAATGAATAGTAGTGAATTAATTAATTAAT 532

RESULT 2

AW759200
 LOCUS 527 bp mRNA linear EST 03-DEC-2001
 DEFINITION s138c06.y1 Gm-cl027 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 Gm-cl027-3587 5' similar to TR:092M42 092M42 F17L21.28. ; mRNA
 sequence.
 ACCESSION AW759200
 VERSION AW759200.1 GI:7691066
 KEYWORDS
 SOURCE
 ORGANISM
 soybean.
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE
 1 (bases 1 to 527)
 Shoemaker R., Kelm P., Vodka L., Erpelting J., Corryell V., Khanna
 A., Bolla B., Merritt M., Hillier L., Kneba T., Martin J., Beck C.,
 Wyllie T., Underwood K., Steptoe M., Theising B., Allen M., Bowers
 Y., Person B., Swaller T., Gibbons M., Pape D., Harvey N., Schurk
 R., Ritter E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann
 R., Waterston R. and Wilson R.
 Public Soybean EST Project
 Unpublished (1999)
 TITLE
 JOURNAL
 COMMENT
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: cdueresgen.com
 Insert Length: 900 Std Error: 0.00
 High quality sequence stop: 435.

FEATURES

source

1..527
 Location/Qualifiers
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl027-3587"
 /clone_1lb="Gm-cl027"
 /tissue_type="cotyledons of 3- and 7-day-old Williams
 seedlings"
 /lab_host="DH10B"
 /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
 xhoI; This cDNA library was constructed from mRNA isolated
 from cotyledons of 3- and 7-day-old Williams seedlings
 which were propagated on paper towels with distilled
 water. The cotyledons were flash-frozen in liquid
 nitrogen, then lyophilized for 72 hours. Unequal amounts
 of mRNA was used for cDNA synthesis. Stratagene's cDNA
 Synthesis Kit (catalog number 200401) was used to
 synthesize the cDNA. First-strand synthesis was
 performed with 5-methyl dCTP, hence the ligated cDNA was
 hemimethylated. A modification of Stratagene's
 first-strand synthesis primer was used. An anchor
 nucleotide (V-A, C, or G) was added to the 3' end of the
 primer [GAGAGAGAGAGAGAGACGACGCTGAG(TT)18] to anchor
 the primer at the 5' end of the poly(A) tract. After
 second-strand synthesis, the cDNA ends were filled in
 with cloned Pfu DNA, ligated to EcoRI adapters and
 subsequently phosphorylated. The XhoI site within the
 first-strand synthesis primer was then restricted by
 digestion with XhoI: all XhoI sites in the cDNA would be
 protected by their hemimethylated status. The cDNA
 constructs were size-fractionated with a 500 bp cutoff,
 using GibcoBRL Life Technologies' cDNA Size Fractionation
 column. The column eluent was then ligated into
 Stratagene's pBluescript(II) M13 digested with EcoRI
 (pBluescript II SK(+)) that has been digested with EcoRI
 and XhoI, and phosphorylated by Stratagene). 97% of the
 white and blue colonies appear to contain recombinant
 plasmids with cDNA inserts, based on size (n=30). This

Library was constructed by Dr. Paul Keim and Dr. Virginia
Coryell."

Query Match 38.7%; Score 515.8; DB 10; Length 527;
Best Local Similarity 98.7%; Pred. No. 1.4e-145;
Matches 520; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 626 TTTCCCACTTTAGAGGCGCTATTGTGCTACACTACTAAAGAACCCCTCTT 685
DB 1 TCTCCACAGTTTAGAGGCGCTATTGTGCTACACTACTAAAGAACCCCTCTT 60
QY 686 GGGCAAAAAATTCATCAACACTTCATGCTCTTTCAGCTCCATGGGCTGTATAG 745
DB 61 GGGCAAAAAATTCATCAACACTTCATGCTCTTTCAGCTCCATGGGCTGTATAG 120
QY 746 ACGAATGTACACCTTGTGATCGGCAACACTTGGAGTCCCTAGTGAACCTTTAT 805
DB 121 ACGAATGTACACCTTGTGATCGGCAACACTTGGAGTCCCTAGTGAACCTTTAT 180
QY 806 TAGTGAGGATGACCAAGAAGCTCCGAGATACCTTTGGCTTTGGCTTAACCCAAAA 865
DB 181 TAGTGAGGATGACCAAGAAGCTCCGAGATACCTTTGGCTTTGGCTTAACCCAAAA 240
QY 866 TTTTGGTCTCAAAAACCAATAGTAACTCAATTAGGCTTTATTCAGCTCATGACA 925
DB 241 TTTTGGTCTCAAAAACCAATAGTAACTCAATTAGGCTTTATTCAGCTCATGACA 300
QY 926 TGGTTGATTTTCTAAAGACATGTTGTTTCTGAAGGGTTTATCTTATGAACACGAA 985
DB 301 TGGTTGATTTTCTAAAGACATGTTGTTTCTGAAGGGTTTATCTTATGAACACGAA 360
QY 986 TTTACCTTGTATGGGACACTAAAGCACACAGTCCCTATTAATCTTGTATGGAA 1045
DB 361 TTTACCTTGTATGGGACACTAAAGCACACAGTCCCTATTAATCTTGTATGGAA 420
QY 1046 CGGAGTGGGAACTTGTTGTTTATGGAAAGGATTTGATGAACGGCCAG 1105
DB 421 CGGAGTGGGAACTTGTTGTTTATGGGAAAGGATTTGATGAACGGCCAG 480
QY 1106 AATATATATATGGGATGTGATGAACGTTGATGGTGG 1152
DB 481 AATATATATATGGGATGTGATGAACGTTGATGGTGG 527

RESULT 3
BM885973 507 bp mRNA linear EST 08-MAR-2002
LOCUS sam10613.y1 Gm-cl063 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-cl063-5158 5' similar to TR:Q9ZM42 Q9ZM42 F17121.28. ; mRNA
sequence.

ACCESSION BM885973
VERSION BM885973.1 GI:19269717
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 507)
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucada, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Stepoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R. and Wilson, R.

TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
1. 507

FEATURES
source
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl063-5158"
/clone_1bp="Gm-cl063"
/lissue_type="Germinating shoot, 24 hour germination"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from germinating shoots of the cultivar Williams. The
seeds were allowed to germinate for 24 hours prior to
harvesting the germinating shoots. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dt) sequence with a xhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by xhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (Gibco BRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker at Iowa state university."

BASE COUNT 145 a 125 c 100 g 137 t
ORIGIN
Query Match 32.4%; Score 432; DB 14; Length 507;
Best Local Similarity 100.0%; Pred. No. 4.6e-120;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGAAGGAACAAGAGGCTCAAGATTGAGTTGCTACACTACAGTTACATA 60
DB 76 ATGAAGAAGGAACAAGAGGCTCAAGATTGAGTTGCTACACTACAGTTACATA 135
QY 61 GTTGTGTGATGCTGTCAATTCATGACATGTGGGCAACCACTGACCTTTGATT 120
DB 136 GTTGTGTGATGCTGTCAATTCATGACATGTGGGCAACCACTGACCTTTGATT 195
QY 121 CTAATACAGGTAACGAGGAGAACCACTAGAACGAGTTGACCAATCAGTACAGCC 180
DB 196 CTAATACAGGTAACGAGGAGAACCACTAGAACGAGTTGACCAATCAGTACAGCC 255
QY 181 TCTACTTTCATCTCGAATCATGTGACCTCTCATCAAGAAAAGATGATGTTGCA 240
DB 256 TCTACTTTCATCTCGAATCATGTGACCTCTCATCAAGAAAAGATGATGTTGCA 315
QY 241 CTTGGTGTGATTCACAGTCACTACTGCTCCTTCACTCAATGTTGGCAAGCATG 300
DB 316 CTTGGTGTGATTCACAGTCACTACTGCTCCTTCACTCAATGTTGGCAAGCATG 375
QY 301 ACCCTTCATTCACCAAGACATGATTAATCAACACTCTCGGGTTGAGACCCGG 360
DB 376 ACCCTTCATTCACCAAGACATGATTAATCAACACTCTCGGGTTGAGACCCGG 435
QY 361 GTCCCTCACTTGGTTCACCAACTCTCTCTATCTCAATCTCTGTCGAAGCATATC 420
DB 436 GTCCCTCACTTGGTTCACCAACTCTCTCTATCTCAATCTCTGTCGAAGCATATC 495
QY 421 ACCGATATCATG 432
DB 496 ACCGATATCATG 507
RESULT 4

BG524903
 LOCUS BG524903 650 bp mRNA linear EST 16-NOV-2001
 DEFINITION 8-8 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
 sequence.
 ACCESSION BG524903
 VERSION BG524903.1 GI:16948350
 KEYWORDS EST.
 SOURCE Stevia rebaudiana.
 ORGANISM Stevia rebaudiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asterales; euasterids II; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Stevia.
 REFERENCE 1 (bases 1 to 650)
 Brande, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.
 Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in
 diterpene synthesis
 JOURNAL Unpublished (2001)
 COMMENT Contact: Jim Brande
 Genomics and Biotechnology
 Agriculture and Agri-Food Canada - SCPPFC
 1391 Sandford St., London, Ontario, CANADA, N5V 4T3
 Tel: 519 457 1470
 Fax: 519 457 3997
 Email: brandeje@em.agr.ca
 Seq primer: T3 promoter primer.
 FEATURES
 source
 1..650
 /organism="Stevia rebaudiana"
 /strain="751/1501"
 /cultivar="Landrace"
 /db_xref="taxon:35670"
 /clone_lib="Stevia field grown leaf cDNA"
 /tissue_type="leaf"
 /dev_stage="field grown, mid-size"
 /lab_host="E. coli strain XL0R"
 /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
 cDNA library was constructed from polyA+ enriched mRNA
 from field grown leaves. Mid-size actively growing leaves
 were collected and pooled from several plants and frozen
 immediately after harvesting in liquid nitrogen. The cDNA
 was prepared using an XhoI-poly(dT) linker-primer. An
 EcoRI adapter was ligated to the blunt end cDNA and the
 products were digested with EcoRI and XhoI enabling
 directional cloning into the lambda Zap Express vector.
 The library was amplified using the host strain XL1-Blue
 MRF. Mass excision of the library was performed to
 obtain pBK-CMV phagemid clones in the host strain XL0R.
 Single pass DNA sequencing was performed using the T3
 promoter primer: 5' ATTAACCTCCTCAAGGA 3'. This library
 was constructed by Alex Richman."

BASE COUNT 171 a 164 c 143 g 171 t
 ORIGIN

Query Match 25.1%; Score 333.8; DB 12; Length 650;
 Best Local Similarity 69.5%; Freq. No. 4.4e-90;
 Matches 452; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

Oy 235 TTCACACTTTGGTTGATTCAGATGTCATACCTGCTTCACATCAATGCTGGCCGA 294
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 TTACAGGCTATGTTGAGAGTCGGCTGTTGTCACACCTTACCGAGCTTTTGGCCAT 60
 Oy 295 CGCATGACCCCTTCATTACCAAGAACTGATTTACTTCAACAGCTCCGTGGTGGAG 354
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 CGTATGAGCGTTACTATGACCGAGATGTCATGATTTACAAAATGTCGCCGAGTGGAG 120
 Oy 335 ACCGCGGTCCTCATCTTGGTTCACCAACTCTTCTCTATCTAATCTGCTCAAG 414
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121 ACTAGAGTGTCTCAGTTGGTCTTACTCATCTCTCTACTCTGATCTCTTTCAAG 180
 Oy 415 CATATCACCGGATGATGACCGCTGGATGATTCATTACAAAGCTGGCAGCTGAT 474
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 CATATACCAACTATGACGACCTTGGTGGATCTTATACACAACTGGCTACAAAGAT 240

Oy 475 GGTGAGACTGCTGTTGGAGCCCTTATGACTTATGATGCTAGCTGTGAAGTCAAC 534
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 ACCGAGAAATCTTTTGGAGCTCCATATGATTTTCTTACGGGTATGACATCCGAAGACAT 300
 Oy 535 CCTTCACAGAGTGGGTTCAGATTTCTTCAAGATCTTAAGAAATTTGATAGAACAGCAAC 594
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 301 CTTTGTGATGTGGGCTCAACTTACCTCCAAAACCTTAACAGCTTAATCGAAAACCAAC 360
 Oy 595 AATTCCAATTAATGGGAAGCAGTACATCTCTCCACAGTTTGGAGAGCCTATTTGTC 654
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 361 AACACAAATGGGGGAGCTCCCGGTGATCTCTGCTCCACAGTCTTGGAGGCTGTTCGCA 420
 Oy 655 CTACAACTACTAATATGAAGAACCCCTCTTGGCGCAAAAATTCATCAACACTTCAT 714
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 421 CTCCAACTCTCAACCGTAACCCACACCTCATGGCGCAAAACATATTAACATTTTATC 480
 Oy 715 GCTCTTTCAGCTCCTATGGGTGGTGTATAGACGAATGTACACCTTTCATCTGGCAAC 774
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 481 GGGTGTCCGACACATGGGGGTGAACGGTGTGACGATGTTAACTTTGCTTGGGAAC 540
 Oy 775 ACTTTGGAGAGTCCCTTACTGAGACCTTATATGAGGAGATGAACAAAGAGCTCCGAG 834
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 541 ACTCTGGAGTTCCTCACTGTGTGAACCCGTTGCTGTGTCAGAAACAGACAGCGAGTCTGAA 600
 Oy 835 ACTAACCTTTGGCTTTTGCTTAACCCAAAATTTTGGTCTCAAAAAC 884
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 601 ACCAATTTATGGCTCATGCCACGAGAAACATTTNCTCACACAGACAC 650

RESULT 5
 LOCUS BE322181
 DEFINITION NF010H12IN1F1101 Insect herbivory Medicago truncatula cDNA clone
 NF010H12IN 5', mRNA sequence.
 ACCESSION BE322181
 VERSION BE322181.1 GI:9195958
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 673)
 Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores
 H.R., Inman, J.T., Weller, J.W. and May, G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula Insect herbivory library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Korth K
 Dept. of Plant Pathology
 University of Arkansas
 217 Plant Science Building, Fayetteville, AR 72701, USA
 Tel: 501 575 5191
 Fax: 501 575 7601
 Email: kthorth@comp.uark.edu
 Medicago Genome Initiative accession: MGI:S:24007
 Insert length: 673 Std Error: 0.00
 Plate: 010 row: H column: 12
 Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
 source
 1..673
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF010H12IN"
 /clone_lib="Insect herbivory"
 /tissue_type="local and systemic leaves"
 /dev_stage="mature"
 /note="Vector: Lambda zap; Library was produced from fully
 expanded M. truncatula leaves of plants fed upon by
 Spodoptera exigua (beet armyworm) for 24 hours. Systemic
 (undamaged leaves from injured plants) and wounded leaves

Db	601	GCGACGCTGGACATCGCGAGCTTTTGGC	629
RESULT 7			
LOCUS	B0855578		
DEFINITION	B0855578	630 bp	mRNA linear EST 14-AUG-2002
ACCESSION	OG827805.yg.abl QG-ABCDI		Lettuce salinas Lactuca sativa CDNA clone
VERSION	OG827805.mRNA sequence.		
KEYWORDS	B0855578		
SOURCE	B0855578.1 GI:22241043		
ORGANISM	EST.		
REFERENCE	Lactuca sativa.		
AUTHORS	Lactuca sativa. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Asterales; euasterids II; Asterales; Asteraceae; Lactucaceae; Lactuca.		
JOURNAL	1 (bases 1 to 630)		
COMMENT	Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K. Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomes.ucdavis.edu/ unpublished (2002) Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel.: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@cdrc.org [michelmore@vegmail.ucdavis.edu] belongs to contig Qc_Ca_contig973, see http://cgpb.ucdavis.edu/ for details.		
plate:	QGB27	row: B	column: 05.

FEATURES	Location/Qualifiers
source	1. .630

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/organism="Lactuca sativa"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="CG827805"
/clone_lib="QG-ABCDI lettuce salinas"
/lab_host="E.coli"
/lab_vector="pBRCNDNA5flab: The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TM6_LIB-QG-ABCDI lettuce salinas
TM6_T150E-Chemical Induction
TM6_SEQ-TG1ACCGGG"

```

Query Match	22.2%	Score	296.2	DB	14	Length	630
Best Local Similarity	66.9%	Pred. No.	1.2e-78				
Matches	421	Conservative	0	Mismatches	208	Indels	0
						Gaps	0

QY 529 GGTACCCCTTCACAAAGGAGGGATTCACAGTCTCTCAAAAGATCTAAAGAAATTGATAGAAAGAA 588

Db 1 GGGGATCTCTTGCGCGCGTGGCTCCACCTTCTCTCCAAAACATPAAAGCAGTTAAATCGAGGAA 60

QY 589 GCACGCAATTCCAAATTAATGGGAAGCCAGTAPACTCTCTCCGACAGTTAGGAGGCGTA 648

Db 61 GCACGTGATTCGAAATGGGTGGAAAAACCCGTATCTCATCTCCCATAGTCTCGGTGGCGCTC 120

QY 649 TTTTCTCCACAACTACTAAATAGAAACCCGCCCTCTGGGCGCAAAAATAATCATCAACAC 708

Db 121 TTGCTCTTCACTCTCTCAACCGCACCCGCTCTGGGGGAACCAATCATPAAAGCAC 180

[illegible]

RESULT	8
BG523648	
LOCUS	
DEFINITION	BG523648 587 bp mRNA linear EST 16-NOV-2001 34-12 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA sequence.
ACCESSION	BG523648
VERSION	BG523648..1 GI:16947068
KEYWORDS	EST.
SOURCE	Stevia rebaudiana.
ORGANISM	Stevia rebaudiana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Asterridae; euasterids II; Asterales; Asteraceae; Asteroideae; Heliantheae; Stevia. 1 (bases 1 to 587).
REFERENCE	Brandle,J.E., Richman,A., Swanson,A.K. and Chapman,B.P. Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in diterpene synthesis unpublished (2001)
JOURNAL	Contact: Jim Brandle
COMMENT	

Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCFPFC
1391 Sandford St., London, Ontario, CANADA, N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: brandtje@em.agr.ca
Seq primer: 73 promoter primer.
Location/Qualifiers
1..587

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/organism="Stevia rebaudiana"
/strain="751/1501"
/cultivar="Landrace"
/db_xref="taxon:55670"
/clone_id="Stevia field grown leaf cDNA"
/tissue_type="leaf"
/dev_stage="field grown, mid-size"
/lab_host="E. coli strain XL04"
/note="Vector: pBR-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA

```


[illegible]

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Oy	166	ATATCGTAAACCCCTCTACTTTTCATCTGCGAATCATGTGATCCCTCTCATCAAGAAAG	225								
Db	175	GCCGAGTATTAAGGGAGACTAGTGGTTGTCTCAACCGGTTCTACCCGCTCAAGAAGATGAG	234								
Oy	226	AATGATGATGTTTCAGACTTTGGTTGATTCAGTGTCTACTTGTCTTTCACCTCAATGC	285								
Db	235	GGGGGGTGGTTCAGGCTATGTTGTCAGAGCGGGCGTGTGTTGGACCAATTGACCCGAGTGT	294								
Oy	286	TTTGGCGAAGCGATGACCTTTCATTAACCCAAAGACTGATGATTACTTCAACACTCCT	345								
Db	295	TTTGGCGATGCTATGATACGGTTTACTATGACCGAGATGTCGATGATTACAAAATGCTGCC	354								
Oy	346	GAGGTGTGAGACCGGGGATGCCCTTCTTGGTTCACCAACTCTCTCTATCTCATCTCT	405								
Db	355	GGAGTGGAGACTAGAGTGTGTCTCAGTTTGGTTTACTCAATCGCTTCTCTACTGATCTCT	414								
Oy	406	CGTCTCAAGCATATCACCGGATACATGACCCCTGGTAGATTCAATTCAAAAGCTTGGC	465								
Db	415	TCTTTCAAGCATATTAACAACATATGGAACCATTTGGTAGATCTATACAAACACTTGGCC	474								
Oy	466	TACGCTGATGTTGAGACACCTGTTTGGAGCCCTTATGATTAAGATATGCTGTAGCTGT	525								
Db	475	TACAAAGATATACCGAAATCTTTTCGAGCTCATATGATTTCGATACGGGTAGCATCC	534								
Oy	526	GAGGTCAACCTTTCACAAGTGGGTTCCAAAGTTCCTCAAGATCTAAAGATTTGATAGAA	585								
Db	535	GAGGACATATCTTGTGATGTGCGCTCAACTTACCTTCACAAACCTTAAGCAGTTAATCGAA	594								
Oy	586	CAGACGACGA 595									
Db	595	AACGCAACGA 604									
RESULT 11											
LOCUS	BG526525	616 bp	mRNA	linear	EST 16-NOV-2001						
DEFINITION	60-13 Stevia field grown leaf cDNA	Stevia rebaudiana cDNA 5', mRNA									
ACCESSION	BG526525										
VERSION	BG526525.1	GI:16950014									
KEYWORDS	EST.										
SOURCE	Stevia rebaudiana.										
ORGANISM	Stevia rebaudiana										
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;										
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;										
TITLE	Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;										
JOURNAL	Helianthus; Stevia.										
COMMENT	1 (bases 1 to 616)										
	Brandle,J.E., Richman,A., Swanson,A.K. and Chapman,B.P.										
	Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in										
	diterpene synthesis										
	Unpublished (2001)										
	Contact: Jim Brandle										
	Genomics and Biotechnology										
	Agriculture and Agri-Food Canada - SCFPFC										
	1391 Sandford St., London, Ontario, CANADA, N5V 4N3										
	Tel: 519 457 1470										
	Fax: 519 457 3997										
	Email: brandleje@em.agr.ca										
	Seq primer: T3 promoter primer.										
	Location/Qualifiers										
	1..616										
FEATURES											
source			</								

from field grown leaves. Mid-size actively growing leaves were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The cDNA was prepared using an XhoI-poly(AT) linker-primer. An EcoRI adapter was ligated to the blunt end cDNA and the products were digested with EcoRI and XhoI enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the host strain XL1-Blue MR⁺. Mass excision of the library was performed to obtain pBR-CMV phagemid clones in the host strain XL0R. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTAACTCTCACTAAAGGCA 3'. This library was constructed by Alex Richman."

BASE COUNT 168 a 117 c 162 g 161 t 8 others
ORIGIN

Query Match

Best Local Similarity 64.4%; Score 216.8; DB 12; Length 616;
Matches 337; Conservative 0; Mismatches 185; Indels 1; Gaps 1;

QY 671 GAATCCCCCTCTGGCGCAAAATTCATCAACACTTATGCTTTCAGCTCAT 730
DB 4 GTAAACCCATCTTCTGCGCAAAATTCATCAACACTTATGCTTTCAGCTCAT 63
QY 731 GGGGTGCTGCTATAGCAAAATTCATCAACACTTATGCTTTCAGCTCAT 789
DB 64 GGGGTGCAACGCTTATAGCAAAATTCATCAACACTTATGCTTTCAGCTCAT 123
QY 790 CTAGTGAACCTTATATAGTGAAGGATGAACAAGAGCTCCGAGATACCTTGGCTT 849
DB 124 CTGCTGAACCTTATATAGTGAAGGATGAACAAGAGCTCCGAGATACCTTGGCTT 183
QY 850 TTGGCTTAACCAAAATTTTGGTCCCAAAACCAATAGATAGTCAATTAAGCCT 909
DB 184 ATGCCACAGCAAAATTTTGGTCCCAAAACCAATAGATAGTCAATTAAGCCT 243
QY 910 TATTCACCTCATGATGATGATTTCTTAAAGACATTTGTTTCCGAGAGGCTTAT 969
DB 244 TATTCACCTCATGATGATGATTTCTTAAAGACATTTGTTTCCGAGAGGCTTAT 303
QY 970 CTTATGAACAGCAATTCATCCCTGATAGGAACATTAAGACCAACAACCTTATA 1029
DB 304 CTTATGAACAGCAATTCATCCCTGATAGGAACATTAAGACCAACAACCTTATA 363
QY 1030 ACTTGTATTTATGGAAGGAGTGGGAACCTTGAACATTTTATGGAAGGAT 1089
DB 364 ACCTGTATTTATGGAAGGAGTGGGAACCTTGAACATTTTATGGAAGGAT 423
QY 1090 TTGATGAACGCGCAGAAATATCATATGGGATGATGATGATGATGATGATGAT 1149
DB 424 TTGATGAACGCGCAGAAATATCATATGGGATGATGATGATGATGATGATGAT 483
QY 1150 TTGTTGGCGCTTCAATCACTATGGAAGAGGAGAAATCAAT 1192
DB 484 TTGTTGGCGCTTCAATCACTATGGAAGAGGAGAAATCAAT 526

RESULT 12
B0864610 527 bp mRNA linear EST 14-AUG-2002
LOCUS OGC27C22.yg.abl OG_ABCDI lettuce salinas Lactuca sativa cDNA clone
DEFINITION OGC27C22. mRNA sequence.
ACCESSION B0864610
VERSION B0864610.1 GI:22250075
KEYWORDS EST.
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; eunasteriids II; Asterales; Asteraceae; Lactuceae;
Lactuca.

REFERENCE 1 (bases 1 to 527)
AUTHORS Kozik,A., Michmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,

TITLE
JOURNAL
COMMENT
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michmore]
Department of Vegetable Crops, R.W.Michmore Lab
University of California at Davis (UCD)
Asmudson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michmore@ucdavis.edu]
singleton, see http://cgpb.ucdavis.edu/ for details.
Plate: OGC27 row: C column: 22.

FEATURES

source

Location/Qualifiers
1..527
/organism="Lactuca sativa"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="OGC27C22"
/clone_id="OG_ABCDI lettuce salinas"
/lab_host="E.coli"
/note="Vector: pBRCDNA51AB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpb.ucdavis.edu/TAG-LIB-OG_ABCDI lettuce salinas TAG-TISSUE-flowers post-fertilized TAG_SEQ-TGCCATCGCG"

BASE COUNT 122 a 125 c 147 g 133 t
ORIGIN

Query Match

Best Local Similarity 68.2%; Score 205.2; DB 14; Length 527;
Matches 285; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 104 ACCGCGACCTTTGATTTATACAGGTAAAGGAGGAGACCACTAGACAGGTTGA 163
DB 110 AGCTTATCCGTTACTTGTGCTCCGTGAGCGGCGGAGACCACTAGACAGGTTGA 169
QY 164 CCATCACTACAAAGCCCTCTACTTTCATCTCGAATCATGTGTACCTCTCAAGAAA 223
DB 170 CGCGGAGTATTAAGGAGCGAGCGGTATGACAGCCGATTTACCAATTAAGAGCAGG 229
QY 224 AGATGATGTTGACACTTGTGTTGATTCAGATGATATCTGCTCTTCACTCAT 283
DB 230 AGGAGGTGTTGCTCGCTATGATGTTGACGTGATTTATGACCACTTCTTGGAGT 289
QY 284 GCTTGGCGAAGCATGACCTTCATTTACCAAGAACTGATGATTTACTTCAACACTC 343
DB 290 GTTTTGTGAAGATGACCTTTACTACACCAAGATTTGATGATTTACAGAAATGCTC 349
QY 344 CTGGGTTGAGACCGGCTCCCTCACTTGTGTTCCACCACTCTCTTCTATCTCAATC 403
DB 350 CGGAGTTGAGACGAGGCTGTGTAGTTGTTTCCACATCACTTCTTCACTGATC 409
QY 404 CTGCTGACATATACCGGATATGACACCCCTGTGATATTCATTAAGAAAGCTTG 463
DB 410 CTAATCTCAACACATTAACGATTAACATGACCACTTGTGAGATCTTCAAGAGCTTG 469
QY 464 GCTACGCTGATGATGAGCTCTGTTTGGAGCCCTTATGATGATGATGATGATGAT 521
DB 470 GCTACCGATTAACAAACATTTGAGAGCACTTACGATTTCCGTTATGAGCTTGC 527

RESULT 13
AV441327/c

[illegible]

QY	1159	CTTCATACACTGGAAGAGAGAAATCAATACCTTAAAGCTGTTAGATAGATGGG	1218
Db	138	TT-----GAAAGTCGATACCTTGAACACCGCTAGCATTTGATGGA	100
QY	1219	GTGTCTACTTCTTCAATAGAGATGAAGTTCGACTTAATGAATAGTAGTGAGATT	1278
Db	99	GTTTCGATACACTTACTTAAACAGCAGATCGACATTAAGAGATTATGAAGCAGATT	40
QY	1279	ACTTCATTAAATCTCA	1295
Db	39	TCAATTATTAAATATGA	23
RESULT 14			
AV827187	LOCUS		
AV827187	600 bp	mrna	linear
AV827187	RAFL9	Arabidopsis thaliana	EST 01-APR-2007
AV827187	DEFINITION		
AV827187	Arabidopsis thaliana cDNA clone RAFL09-12-E12 5', mRNA sequence.		
AV827187	VERSION		
AV827187.1	GI:19869247		
AV827187	KEYWORDS		
AV827187	EST.		
ORGANISM	thale cress.		
ORGANISM	Arabidopsis thaliana		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 600)		
REFERENCE	Seki, M., Narusaka, M., Ishida, J., Kamuya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.		
REFERENCE	Large scale analysis of Arabidopsis full-length cDNA (2002b)		
REFERENCE	Unpublished (2002)		
TITLE	Contact: Motoaki Seki		
JOURNAL	Plant Functional Genomics Research Group		
COMMENT	RIKEN Genomic Sciences Center		
COMMENT	3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan		
COMMENT	Tel: 81-298-36-4359		
COMMENT	Fax: 81-298-36-9060		
COMMENT	Email: mseki@r.riken.go.jp		
COMMENT	An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified lambda FliC1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/Plant/index_e.html) for further details.		
FEATURES	Location/Qualifiers		
source	1..600		
source	/organism="Arabidopsis thaliana"		
source	/db_xref="taxon:3702"		
source	/clone="RAFL09-12-E12"		
source	/clone_id="RAFL9"		
source	/dev_stage="plants at various developmental stages from germination to mature seeds"		
source	/lab_host="DH10B"		
source	/note="Site_1: BamHI. Site_2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"		
BASE COUNT	158 a 129 c 136 g 174 t 3 others		
ORIGIN			
Query Match	12.9% Score 171.6; DB 10; Length 600;		
Best Local Similarity	62.7% Pred. No. 1.e-40;		
Matches 299; Conservative	0; Mismatches 172; Indels 6; Gaps 2;		
QY	45	ACGTACAGTTACAGAGTGTGGATCTCTGCATGTCGTAGCAGATGGGCAAGCA	104
Db	124	AGTACATACGATCTCGTTGGTGACATACCTCGATGTGTCAAGCTGTGGGTAGCA	183
QY	105	CCGTGACCTTTGATTCTTAATACAGGTAAAGGAGGAGCAACATAGAGCAAGTTGAC	164

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 19:11:35 ; Search time 40 Seconds
(without alignments)
1475.751 Million cell updates/sec

Title: US-09-857-612A-14

Perfect score: 2333
Sequence: 1 MKKEQEGKLEIVATLVTV.....GETTSINSHALGSLNFSG 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

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3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2333	100.0	443	21	soybean putative 1
2	2022	86.7	381	21	soybean putative 1
3	1380.5	59.2	432	21	Arabidopsis thalia
4	1380.5	59.2	432	21	Arabidopsis thalia
5	1380.5	59.2	432	21	Arabidopsis thalia
6	1380.5	59.2	432	21	Arabidopsis thalia
7	1380.5	59.2	432	21	Arabidopsis thalia
8	1367	58.6	413	21	Arabidopsis thalia
9	1367	58.6	413	21	Arabidopsis thalia
10	1366	58.6	410	21	Arabidopsis thalia

11	1366	58.6	410	21	AA642648	Arabidopsis thalia
12	1345	57.7	387	21	AA624263	Arabidopsis thalia
13	913.5	39.2	417	21	AA601209	Corn putative leci
14	739.5	31.7	439	21	AA601210	Corn putative leci
15	717	30.7	434	21	AA601208	Corn putative leci
16	612	26.2	412	19	AA680944	Murine kidney leci
17	610	26.1	412	19	AA680942	Human heart leci
18	610	26.1	412	20	AA641708	Human PRO540 prote
19	610	26.1	412	21	AA644264	Human PRO540 (UNQ3
20	610	26.1	412	21	AA619579	Human PRO540 used
21	610	26.1	412	22	AA693359	Human polypeptide,
22	610	26.1	412	22	AA693243	Human protein sequ
23	610	26.1	412	22	AA650954	Human PRO540 prote
24	610	26.1	412	23	AB634036	Human Pro peptide
25	608	26.1	379	19	AA680937	Human heart leci
26	608	26.1	382	19	AA680940	Human heart leci
27	606	26.0	379	19	AA680939	Murine leci
28	596	25.5	444	19	AA680943	Human kidney leci
29	594	25.5	411	19	AA680938	Human kidney leci
30	594	25.5	414	19	AA680941	Human kidney leci
31	560	24.0	421	19	AB67428	Drosophila melanog
32	543	23.3	440	8	AA670134	Natural recombinan
33	541	23.2	440	18	AA624789	Human leci
34	541	23.2	440	20	AA649562	Human leci
35	541	23.2	440	22	AA672627	Human leci
36	541	23.2	440	23	AA697745	Human leci
37	541	23.2	440	23	AA684290	Human leci
38	541	23.2	440	23	AA651918	Human leci
39	518.5	22.2	318	21	AA691645	Anti-ICAT antibody
40	493	22.1	187	21	AA618062	P. radiata leci
41	421.5	18.1	233	21	AA601206	Corn putative leci
42	376	16.1	117	21	AA618125	P. radiata leci
43	368.5	15.8	143	21	AA601205	Corn putative leci
44	225	9.6	281	22	AB627613	Novel human diagno
45	222.5	9.5	447	22	AA600461	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
ID	AA601211
	AA601211 standard; Protein; 443 AA.
AC	AA601211;
DT	12-DEC-2000 (first entry)
DE	soybean putative leci
KW	soybean: leci
KW	phosphatidylcholine-sterol O-acetyltransferase; heat shock; cold shock.
OS	Glycine max.
PN	WO200032791-A2.
XX	08-JUN-2000.
XX	02-DEC-1999; 99WO-US28586.
XX	03-DEC-1998; 98US-0110782.
XX	(DUPO) DU PONT DE NEMOURS & CO E. I.
XX	Cahoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JT;
XX	WPI: 2000-412337/35.
XX	N-PSDB: AAA49206.
XX	Polynucleotide encoding plant leci
XX	enzyme useful for producing transgenic plants and for producing
XX	antibodies specific to which is useful for screening cDNA expression

PT Libraries -
XX
PS Claim 10: Page 46-47; 49pp; English.
XX
CC The present sequence is a putative protein sequence of a soybean
CC lecithin:cholesterol acyltransferase (also known as
CC phosphatidylcholine-sterol O-acyltransferase). This enzyme is found
CC associated with high-density lipoproteins and Apolipoprotein-AI and -D.
CC The gene and protein can be used to produce transgenic plants which have
CC increased lipid metabolism and membrane fluidity, and therefore increased
CC resistance to heat and/or cold shock, to alter the content of phytosterol
CC or lecithin in grains and to identify potential herbicides.
XX
SQ Sequence 443 AA;

Query Match 100.0%; Score 2333; DB 21; Length 443;
Best Local Similarity 100.0%; Pred. No. 4.1e-219;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKQEGELKIEVATLVTVVVMVLSLCTCGASNLDPILIPGNGNQLBARLTNOYKP 60
Db 1 MKKQEGELKIEVATLVTVVVMVLSLCTCGASNLDPILIPGNGNQLBARLTNOYKP 60
QY 61 STFCESWYPLIKKNGWFLMFDSSVILAFPTQCFARMTLHYHQELDDYFNTPGVETR 120
Db 61 STFCESWYPLIKKNGWFLMFDSSVILAFPTQCFARMTLHYHQELDDYFNTPGVETR 120
QY 121 VPHGGSNLSILYNPRLKHTGYMAPLVDSLOKLGADGETLFGAPYDFRYGLAEGHPS 180
Db 121 VPHGGSNLSILYNPRLKHTGYMAPLVDSLOKLGADGETLFGAPYDFRYGLAEGHPS 180
QY 181 QVGSKFLDKNLIEASNSNNGKPVILLSHSLGFLVQLNRPSPMRKFKIKHFIAL 240
Db 181 QVGSKFLDKNLIEASNSNNGKPVILLSHSLGFLVQLNRPSPMRKFKIKHFIAL 240
QY 241 SAPMGAIIDEMYTFASGNTLGVPLVDPLVDRDQRSSSNMLLPPNKIFGPQPIVITP 300
Db 241 SAPMGAIIDEMYTFASGNTLGVPLVDPLVDRDQRSSSNMLLPPNKIFGPQPIVITP 300
QY 301 IRPASHDMVDFLKDIGFPEGVYPERTRILPLIGNIKAPQVPTTCIMGTGVTLETLYFG 360
Db 301 IRPASHDMVDFLKDIGFPEGVYPERTRILPLIGNIKAPQVPTTCIMGTGVTLETLYFG 360
QY 361 KGDERPEREISYGDGDTVNLVSLALQSLMKKEKNQYLKVVKIDGVSHTSILKDEVALN 420
Db 361 KGDERPEREISYGDGDTVNLVSLALQSLMKKEKNQYLKVVKIDGVSHTSILKDEVALN 420
QY 421 EIVGEITSINSHAEGLSNLFSG 443
Db 421 EIVGEITSINSHAEGLSNLFSG 443

RESULT 2
AAB01207
ID AAB01207 standard; Protein: 381 AA.
XX
AC AAB01207;
XX
DT 12-DEC-2000 (first entry)
XX
DE Soybean putative lecithin:cholesterol acyltransferase #1.
XX
KM Soybean: lecithin:cholesterol acyltransferase; phytosterol;
KM phosphatidylcholine-sterol O-acyltransferase; heat shock; cold shock.
XX
OS Glycine max.
XX
PN MO200032791-A2.
XX
PD 08-JUN-2000.
XX
PF 02-DEC-1999; 99MO-US28586.
XX

PR 03-DEC-1998; 98US-0110782.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
PI Cahoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;
XX
DR WPI: 2000-412337/35.
XX
DR N-PSDB: AAA49202.
XX
PT Polynucleotide encoding plant lecithin:cholesterol acyltransferase
PT enzyme useful for producing transgenic plants and for producing
PT antibodies specific to which is useful for screening cDNA expression
PT libraries -
PS Claim 10: Page 38-39; 49pp; English.
XX
XX The present sequence is a putative protein sequence of a soybean
CC lecithin:cholesterol acyltransferase (also known as
CC phosphatidylcholine-sterol O-acyltransferase). This enzyme is found
CC associated with high-density lipoproteins and Apolipoprotein-AI and -D.
CC The gene and protein can be used to produce transgenic plants which have
CC increased lipid metabolism and membrane fluidity, and therefore increased
CC resistance to heat and/or cold shock, to alter the content of phytosterol
CC or lecithin in grains and to identify potential herbicides.
XX
SQ Sequence 381 AA;

Query Match 86.7%; Score 2022; DB 21; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.4e-189;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 FICSWYPLIKKNGWFLMFDSSVILAFPTQCFARMTLHYHQELDDYFNTPGVETR 122
Db 1 FICSWYPLIKKNGWFLMFDSSVILAFPTQCFARMTLHYHQELDDYFNTPGVETR 122
QY 123 HFGSTNSILYNPRLKHTGYMAPLVDSLOKLGADGETLFGAPYDFRYGLAEGHPSQV 182
Db 61 HFGSTNSILYNPRLKHTGYMAPLVDSLOKLGADGETLFGAPYDFRYGLAEGHPSQV 182
QY 183 GSKFLDKNLIEASNSNNGKPVILLSHSLGFLVQLNRPSPMRKFKIKHFIALSA 242
Db 121 GSKFLDKNLIEASNSNNGKPVILLSHSLGFLVQLNRPSPMRKFKIKHFIALSA 180
QY 243 PMGGAIDEMYTFASGNTLGVPLVDPLVDRDQRSSSNMLLPPNKIFGPQPIVITP 302
Db 181 PMGGAIDEMYTFASGNTLGVPLVDPLVDRDQRSSSNMLLPPNKIFGPQPIVITP 302
QY 303 PYSAHDMVDFLKDIGFPEGVYPERTRILPLIGNIKAPQVPTTCIMGTGVTLETLYFG 362
Db 241 PYSAHDMVDFLKDIGFPEGVYPERTRILPLIGNIKAPQVPTTCIMGTGVTLETLYFG 300
QY 363 DFDERPEREISYGDGDTVNLVSLALQSLMKKEKNQYLKVVKIDGVSHTSILKDEVALNEI 422
Db 301 DFDERPEREISYGDGDTVNLVSLALQSLMKKEKNQYLKVVKIDGVSHTSILKDEVALNEI 360
QY 423 VGEITSINSHAEGLSNLFSG 443
Db 361 VGEITSINSHAEGLSNLFSG 381

RESULT 3
AAB24260
ID AAB24260 standard; Protein: 432 AA.
XX
AC AAB24260;
XX
DT 12-FEB-2001 (first entry)
XX
DE Arabidopsis thaliana PDAT amino acid sequence SEQ ID NO:14.
XX
KM PDAT: phospholipid:diacylglycerol acyltransferase; triacylglycerol;
KM TAG; EST: expressed sequence tag; fatty acid; oil content.
XX

[illegible][illegible]


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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 11-AUG-1999; 99US-0148319.
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PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
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PR 01-SEP-1999; 99US-0151930.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 59.2%; Score 1380.5; DB 21; Length 432;
Best Local Similarity 61.0%; Pred. No. 5.3e-126;
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QY 1 MKKEDEEGKIEVATITVVVYVMSLCTCCASNDPLILIPGNGNOLFARTLQNYRP 60
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MKK-----ISSHSYVIALIVVYTMSTMCOAVGSNNYPLILVPGNGNOLFARLDEYRP 55
QY 61 STFICESS-YPLIKKNGWFRLEFSSVTLAPTOCFARMTLHYHQELDDYFNPFGVEF 119
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
56 SSYWCSSMLYPLIHKKSGGFRLEFDNAVILSPFTKCFSRMLLYDPDDLDYQNAFGVQT 115
DB 120 RVPHEGFSNLLYLNEPLRLHITGYMAPLVDSIQ-KIGYADGETLFGAPYDFRYGLAEGH 178
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
116 RVPHEGSTSLLYDLRLDATSMEHLVKALEKKGYNVDITIGAPDFRGLAASGH 175
QY 179 PSQVSGKFLKDLKNLIEEASNSNNGKPVLLSHSLGGLVVLQLLNPNPSMRKKFTIKHT 238
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
176 PSRVASQFLDQLKQLEKTSSENEGKPVILLSHSLGGLVFLIHNTPSPWRKRYIKHIV 235
QY 239 ALSAPWGAIDEMVTFASNTLGVPLVDPLVLRDEQRSSSNMILNPKIKGPO-KPIY 297
||:||||| : : | ||||| : : : : : : : : : : : : : : : : : : : :
236 ALAAPWGTTISQKTFASNTLGVPLVPLVRRHORISESNOMLLPSTKVRHDKTKPLV 295
QY 298 ITPIRYSADHWDFELKDIFPEGVYVYETRLPLIGNIKAPQVPITCMTGCGTLETL 357
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296 VTPQVNYTAYENDRFFADIGFSGVVPYKTRVLPLLELMTFGVPVTCYGRGVDPREVL 355
DB 358 FYGKGDEDERPEISYGDGTYNLVSLALQSLKWEKNQYKVKKIDGVSHTSIKDEV 417
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356 MYKGGGFDPKQPEIKYDGDGTWNLSIALV-----KVDLSLNTVYIDGVSHTSIKDEI 408
QY 418 ALNEIYGETSTIN 430
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DB 409 ALKEIMKOISTIN 421

RESULT 6
AAG42646
ID AAG42646 standard; Protein; 432 AA.
XX
AC AAG42646;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53209.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 26-AUG-1999; 99US-0150884.
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PR 07-SEP-1999; 99US-0152363.
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PR 15-SEP-1999; 99US-0154039.
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Oy 418 ALNEIWEITSIN 430
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Db 409 ALKEIMKOISTIN 421

RESULT 8
AAG22980
ID AAG22980 standard; Protein: 413 AA.
XX AAG22980;
AC
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26115.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 10-SEP-1999; 99US-0153070.
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Query Match 58.6%; Score 1367; DB 21; Length 413;
Best Local Similarity 63.1%; Pred. No. 1e-124;
Matches 258; Conservative 58; Mismatches 83; Indels 10; Gaps 4;

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Db 1 WISMCQAVGSNNYPLILVFGNGNGOLEVRLDREYKRPSSVWCSSWLYPIHKKSGGWRLLWF 60

Qy 84 DSSVILAPFTOCFAERMTLHYHOELDDYFNTPGVTRVPHFGSTNSLXYLNPLKXITGY 143
Db 61 DAAVLSPTTRCFSDMMMLTYDPDLDDYONAPGVQTRVPHFGSTKSLDLPRLRATSY 120
Qy 144 MAPLVDSLO-KLGYADGETLFGAPDYFRYGLAEGHPQVSGSKFLDKNLJEASNSNN 202
Db 121 MEHLVAKLEKKCGYVNDQITLGAIFYFRYGLAASGHPRSRASFDDLQVLKETSSENE 180
Qy 203 GKPVILLSHSLGGLFVQLLNRPSPWRKKFKHFIKALSAPOGCAIDEMYTRFASGTLY 262
Db 181 GKPVILLSHSLGGLFVQLLNRPSPWRKKFKHFIKALSAPOGCAIDEMYTRFASGTLY 240
Qy 263 PLVDPLLVDEORSSSENNLWLPNPKIFGPQ-KPIYTPIRPSAHDMVDPLKDIGEPFG 321
Db 241 PLVNPPLVRRHQRTHSENNMLPSTVFEDRKPLVVTPOVNTYATEMDRFRADIGFSOG 300
Qy 322 VVPEYTRILPLIGNIKAPOVPIPCINGVGTLLETLYFGKGFDEDERPEISYGGDGTVM 381
Db 301 VVPEYKTRVPLPTEBELMTPGVPTCIYRGVDPEVILMVGKGGPKQPEIKYGGDGTVM 360
Qy 382 VSLAQSILMKERKNQYKLVKIDGVSHTSIKDEVALNEIYEITSIN 430
Db 361 ASIAL------KVDLSMTVEIDGVSHTSIKDEITALKEIMQIISIN 402

RESULT 9
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ID AAG42647 standard; Protein; 413 AA.
XX AAG42647;
AC XX
XX 18-OCT-2000 (first entry)
DT XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53210.
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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OS Arabidopsis thaliana.
OS
PN EP1033405-A2.
PN XX
PD 06-SEP-2000.
PD XX
XX 25-FEB-2000; 2000EP-0301439.
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Query Match	58.6%;	Score 1367;	DB 21;	Length 413;
Best Local Similarity	63.1%;	Pred. No. 1e-124;		
Matches 258;	Conservative 58;	Mismatches 83;	Indels 10;	Gaps 4

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QY	84	DSVVLIAPTCOFAERMTLHVHOELDDYFMTPGVETVPVPHRGSYNSLJLYINPLRKHITGY	143
Db	61	DAVILSPFTRCFSDRMILYDPLDDYQANAPGVQTVPHRGSFKSLIYDLRRLDSTY	120
QY	144	MAPLYDSIQ-KLGYADGETLEFGAPYDTRYGLAAGHPSOVQSKFLDKLNLIEFASNSN	202
Db	121	MEHLVKALEKKCGVNOQTILGAYDPRYGLAAGHPSRAISOPLDKOLVEXTSESENE	180
QY	203	GKPYILISHSGJFVJQOLNRPNSMRKKIKHFIILASAPWGCAIDEMTFASGNLTGY	262
Db	181	GKPYILISHSGJFVJLHFLRTPNSMRKKIKHFVALAAPWGSTISOMTFASGNLTGY	240
QY	263	PLVPLVLVRDEORSSESINMLIPKJFEQP-KPVTTPRIPYFAHMOVFLKIGPEEG	321
Db	241	PLVPLVLVRRIQRKSESNOHMLPSTKFFHDKTRKLVTPPOVNTIAYEMDRFPADIGFSQG	300
QY	322	VVPYETRIPLIGNIKAPQVPTICMGTGVTLETFYFGKDDPEREPIYSXGDDGVNLT	381
Db	301	VVPYKTRVLPTEBLMPGVAVTCIYRGVDTPEVLMYGGKGGPQGEIKYGGSDGVNLT	360
QY	382	VSLLASLGSMEKKNQYLKVKIDGVSHTSIADKDEVALNELVGEITSIN	430
Db	361	ASIAL-----KVDISLNVVEIDGVSHTSILKDEIKELIKEMKISIN	402

XX	RESULT 10
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ID	AAAG22981 standard; Protein; 410 AA.
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AC	AAAG22981;
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DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 26116.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
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PE	25-FEB-2000; 2000EP-0301439.
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PR	23-MAR-1999; 9905-0125788.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
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PR 13-AUG-1999; 99US-0148365.
PR 13-AUG-1999; 99US-0148684.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.

PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161982.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.6%; Score 1366; DB 21; Length 410;
Best Local Similarity 63.5%; Pred. No. 1,3e-124;
Matches 258; Conservative 56; Mismatches 82; Indels 10; Gaps 4;

QY 28 LCTCGASMLDPLILIPGNGNQLBARLNOYKPSFICESEV-YPLIKKNGMFLMDSS 86
Db 1 MCGAVGSMVYPLILVPGNGNQLVRLDREYKPSVMCSMWLYPLHKSGGMFLMDAA 60

QY 87 VILAFPGCFARMTLHNOELDDYFNPGVETRVPHGSGNSLLYLNPRLKHITGYAP 146
Db 61 VILSPFTFCFSDRMQLLYDDPLDDYQNAVGQVTRVPHGSGTKSLYLDPLRLDATSYMEH 120

QY 147 LVDSIQ-KLGYADETTEFGARYDFRYGLAAGHPHSOVGSKFLDKLNLEBASNSNNGKP 205
Db 121 LVKALEKKGTYVNOTLIGARPYDFRYGLAAGHRSRVAQPLDLKQVETSSENEKP 180

QY 206 VILLSHSLGGLFVLQLLRNPPSMKKFKIHFIALSAFWSGALDEMTFASGNTLGYPLV 265
Db 181 VILLSHSLGGLFVHLNRTPTPSWRKKYIKHFVLAAPWGSTISQMKTFASGNTLGYPLV 240

QY 266 DPLVLRDQRSESNLMLPNPKITFGPQ-KPIVITPPIRYSAHDMVDFLKIIGPEGYYP 324
Db 241 NPLVLRHQRTESENQWLLPSTKVFHDTPKPLVYTPVYNVAYEMDRFADIGFSQGVYP 300

QY 325 YETRIPLPLIGNIKAPQVETICMGVGTLETFYKGDPEDEPEISYGDGTVNLVSL 384
Db 301 KTRVLPPLTEELMPGVVETCIYGRGVPTPEVLWKGGKGFQKOEIKKGGDDGTVNLASTL 360

QY 385 LALQSLMKERKNQYLKVVKIDGVSHTSILKDEVALNEIVGETSIN 430
Db 361 AAL-----KVDSLNFVEIDGVSHTSILKDEIKLKEIMKQISLIN 399

RESULT 11
AAG42648
ID AAG42648 standard; Protein: 410 AA.
XX
AC AAG42648;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53211.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX

OS Arabidopsis thaliana.
XX
PN EPI03405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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PR 01-JUN-1999; 99US-0137222.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
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PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
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PR 20-JUL-1999; 99US-0144352.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145088.
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PR 22-JUL-1999; 99US-0145087.
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PR 23-JUL-1999; 99US-0145195.
PR 23-JUL-1999; 99US-0145218.
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PR 26-JUL-1999; 99US-0145276.
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PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
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PR 09-AUG-1999; 99US-0147935.
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PR 12-AUG-1999; 99US-0148341.
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PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.

PR	15-SEP-1999;	990S-0154018.
PR	16-SEP-1999;	990S-0154039.
PR	20-SEP-1999;	990S-0154079.
PR	22-SEP-1999;	990S-0155139.
PR	23-SEP-1999;	990S-0155486.
PR	24-SEP-1999;	990S-0155659.
PR	28-SEP-1999;	990S-0156458.
PR	29-SEP-1999;	990S-0156596.
PR	04-OCT-1999;	990S-0157117.
PR	05-OCT-1999;	990S-0157753.
PR	06-OCT-1999;	990S-0157865.
PR	07-OCT-1999;	990S-0158029.
PR	08-OCT-1999;	990S-0158232.
PR	12-OCT-1999;	990S-0158369.
PR	13-OCT-1999;	990S-0159293.
PR	13-OCT-1999;	990S-0159294.
PR	13-OCT-1999;	990S-0159295.
PR	14-OCT-1999;	990S-0159329.
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PR	14-OCT-1999;	990S-0159638.
PR	18-OCT-1999;	990S-0159584.
PR	21-OCT-1999;	990S-0160741.
PR	21-OCT-1999;	990S-0160767.
PR	21-OCT-1999;	990S-0160768.
PR	21-OCT-1999;	990S-0160770.
PR	21-OCT-1999;	990S-0160814.
PR	21-OCT-1999;	990S-0160815.
PR	22-OCT-1999;	990S-0160980.
PR	22-OCT-1999;	990S-0160981.
PR	22-OCT-1999;	990S-0160989.
PR	25-OCT-1999;	990S-0161404.
PR	25-OCT-1999;	990S-0161405.
PR	25-OCT-1999;	990S-0161359.
PR	26-OCT-1999;	990S-0161360.
PR	26-OCT-1999;	990S-0161361.
PR	28-OCT-1999;	990S-0161920.
PR	28-OCT-1999;	990S-0161992.
PR	28-OCT-1999;	990S-0161993.
PR	29-OCT-1999;	990S-0162142.

Query Match 58.6%; Score 1366; DB 21; Length 410;
Best Local Similarity 63.5%; Pred. No. 1.3e-124;
Matches 258; Conservative 56; Mismatches 82; Indels 10; Gaps 4;

OY	28	LCTGASLNDPLILIPGNGNQLRLTNQYKPSFTICEBW-YPLIKKNGFRLMFDSS	86
DB	1	MCQAVGSNYYPLILVPGNGNQLRLDREYKPPSSVWCSMLYPIHKKSQWFLMFDNA	60
OY	87	VLLAFPTLCFAERMTLHQLDLDYFNTPGVETRYPHGSGTNSLLYLNRLKHIITGYMAP	146
DB	61	VLLSPTKCFSDRMALYDDPLDDYQNAAGVQTRVPHFGSTKSLLYLDRDATSYMEH	120
OY	147	LYDSHQ-KLGYADGETLFGAPYDFRYGLAEGHPQVSGSKFLDKNLIEASNSNNGKP	205
DB	121	LVKALEKKCGYVNDQTIIGAPYDFRYGLAEGHPSRVASQFLQDLKQLVKETSSENECKP	180
OY	206	VLLSHSLGGLFVLQLLNRNPPSRKKFKIHFIALSAPMGAIDEMVTFFASGNTLGVPVY	265
DB	181	VLLSHSLGGLFVLHFLNRTPSMRKYIKHFVALAAMPGTIISQMKTFASGNTLGVPVY	240
OY	266	DPLVLRDQSRSSNLMLNPNKITGPQ-KPIVITPIRIRYSHADWDLKIDGFEQYVP	324
DB	241	NPLLRHQRRTSESQMLLPSTKYFHDRTKPLVTPPVNATYENDREFADIGFSQGVVP	300
OY	325	YETRLPLIGNIKARQVQVITCMGTGVTLETFYKSGDEDERPEISYGGDGTNVLVS	384
DB	301	YKTRPLPLTEELMTGCVPTCTYGRGVDTPEVLMKGKGFDPQPIKIGDGGTIVLASL	360
OY	385	LALQSLMKEEKNOYLKVKIDGVSHTSILKDEVALNEIVGETTSIN	430

DB	361	AAL-----KVDSINTVEIDGVSHTSILKDEIALKEIMKQISIN	399
RESULT 12			
ID	AAB24263	standard; Protein; 387 AA.	
XX	AAB24263;		
AC	AAB24263;		
XX	12-FEB-2001 (first entry)		
DE	Arabidopsis thaliana PDAT amino acid sequence SEQ ID NO:2a.		
XX	PDAT: phospholipid:diacylglycerol acyltransferase; triacylglycerol;		
XX	TAG; EST; expressed sequence tag; fatty acid; oil content.		
OS	Arabidopsis thaliana.		
XX	WO20060095-A2.		
PN	12-OCT-2000.		
PD	28-MAR-2000; 2000WO-EP02701.		
XX	01-APR-1999; 99EP-0106656.		
XX	10-JUN-1999; 99EP-0111321.		
PR	07-FEB-2000; 2000US-0180687.		
XX	(BADI) BASF PLANT SCI GMBH.		
PI	Dahlqvist A, Stahl U, Lenman M, Banaas A, Ronne H, Slymne S;		
XX	WPI; 2000-665012/64.		
DR	Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic		
PT	pathway for triacylglycerol production and DMS encoding them, useful		
PT	for producing triacylglycerol, or for transforming any cell or organism		
XX	to increase oil content -		
PS	Claim 5; Page 68-69; 97pp; English.		

The present invention describes an enzyme for catalysing (in an acyl-CoA-independent reaction) the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol (TAG). The enzyme is designated as phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the nucleotides encoding them are useful for producing TAG and/or TAG with uncommon fatty acids. The enzyme and the nucleotide are also useful for transforming any cell or organism in order to be expressed in this cell or organism and result in an altered, preferably increased oil content of this cell or organism. The present sequence represents an Arabidopsis thaliana PDAT amino acid sequence.

Sequence 387 AA;

Query Match 57.7%; Score 1345; DB 21; Length 387;
Best Local Similarity 64.8%; Pred. No. 1.3e-122;
Matches 254; Conservative 52; Mismatches 76; Indels 10; Gaps 4;

OY	34	SMLDPLILIPGNGNQLRLTNQYKPSFTICEBW-YPLIKKNGFRLMFDSSYILAF	92
DB	3	SNVYPLILVPGNGNQLRLDREYKPPSSVWCSMLYPIHKKSQWFLMFDNAVLSPF	62
OY	93	TQCFARERMTLHQLDLDYFNTPGVETRYPHGSGTNSLLYLNRLKHIITGYMAP	152
DB	63	TRCFSDRMALYDDPLDDYQNAAGVQTRVPHFGSTKSLLYLDRDATSYMEH	122
OY	153	-KLGADETFLEGAHYDPRYGLAEGHPSQVSGSKFLDKNLIEASNSNNGKPVITLISH	211
DB	123	KKCGYVNDQTIIGAPYDFRYGLAEGHPSRVASQFLQDLKQLVKETSSENECKP	182
OY	212	SLGGLFVLQLLNRNPPSRKKFKIHFIALSAPMGAIDEMVTFFASGNTLGVPVPLVLR	271

QY 79 FRLWEDSSVIL-APFTQCEAERM TLHYHQELDDYFNTPGVETRVPHFGSTNSLLYLNPR L 137

Sequence 439 AA;

Query Match	31.7%;	Score 739.5;	DB 21;	Length 439;
Best Local Similarity	41.6%;	Pred. No. 2.6e-63;		

Db 255 GGYRLMAGVDLGFPGAGYGRVDRKPLLVYVYGRPRDPLVTRDEARSLAS 301

RESULT 4
US-08-485-938A-33
Sequence 33, Application US/08485938A
Patent No. 5847088

GENERAL INFORMATION:

APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Toelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/318,905

FILING DATE: 06-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,803

FILING DATE: 06-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5847088and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/32792

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-485-938A-33

Query Match

Best Local Similarity 4.2%; Score 97.5; DB 2; Length 444;

Matches 54; Conservative 39; Mismatches 85; Indels 63; Gaps 10;

Db 189 DKNLIEASNSNNGKPVILLSHSGLFVLQLLNRPSPWKKKFKHIALSA---PVG 245

Db 251 DLEFDEQAKSIDRKIAIIGHSGFATVIGTLESD---ORF-RGCIADAMFPG 304

Qy 246 GAIDEMVTFASNTGLVPLVDLVLVDEQSSSNMLLPNPKIFGPKPIVTPRPYS 305

Db 305 ---DEVY-----SRIPQL---FFINSEFQYPSN---IIRMKCFIPDR----- 340

Qy 306 AHDWVFLKIDGFPBGVYVETRIILPLIGNIKAPQVPTICMGTVGLTETLYFGKDPD 365

Db 341 ---ERKMITIRGSHVQNFVDFTFANSKIGLYFTL---KGIDID 377

Qy 366 ERPEISYGGDGTVMVLSLALQ-----SLMKERKNQYLVKVIDGVSHSILKDEVA 418

Db 378 SNAIISLSKASIAFLQKHLGLQKDPDQWDSLVESGDHNLIPGTINTNTNHQALLQNSRG 437

Qy 419 L 419

Db 438 I 438

RESULT 5

US-09-453-702B-257

Sequence 257, Application US/09453702B

Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.
Burland, Nicole T.
Perna, Valerie
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESS: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-Dec-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296, 95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 257:

SEQUENCE CHARACTERISTICS:

LENGTH: 3169 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 257:

US-09-453-702B-257

Query Match

Best Local Similarity 4.1%; Score 95.5; DB 4; Length 3169;

Matches 87; Conservative 62; Mismatches 152; Indels 149; Gaps 23;

Db 50 LEARLQNRKPSFICSEWPLIKKNGFRMLFDSVILAPPTQCFARMLTHYQELD 109

Db 2716 LEKKNNSYKISKFTWETV-----GDIYVSP-----EDRIS---HLELD 2751

Qy 110 ---DYENTPVEYRV-----PHFGSTNS-----LLYINPRLKHTGYMAPL---VDS 150

Db 2752 GRYVESQPELDIPISDSFYLVDNFQIVSDVHIKILHLNREKQITTPRIILKRFIDS 2811

Qy 151 LQKLYADE---TLFGAP-----YDFRYGLAEG--HPSQVSGSKFLK----- 188

Db 2812 FAKTSTIDREKNINYPICSDPHFTSDIYRHPFRIVLGNKTLVPSSELYKFIKSTSEYLS 2871

Qy 189 -----DKNLIEASNSNNGKPVILLSHSGLFVLQLLNRPSPWKKKFI 234

Query Match	3.9%;	Score 92;	DB 1;	Length 444;
Best Local Similarity	20.5%;	Pred. NO. 0.58;		
Matches 98;	Conservative 51;	Mismatches 122;	Indels 208;	Gaps 26

OY	26	SLLCTCGA-----SNLPLLIPNG-GGNLEARTLYQKSPFICSSWPLIKK	75
Db	8	ALFCLSCSLTLVHPIWMODLVPAHHIRSAANKIQLAMA-----ASTROSRID--KG	59
OY	76	NGMFR---LMFDSSVILAFPTCCFAERMT--LHVHOELDD-	11
Db	60	NGSYSGCTDLMFD-----YTNRGFTLRLYTYPQSDHDSDHTLMIENKEYFGLS	10
OY	111	-YFNTPGVETRP--HFGSTNSLLYLNRKLHITGYAPLVYDSLCKLG-----	15
Db	109	KLTGPMLMGKILSFSEGSVTTPANWNSPLR--TGEEKYPLIVESHGLAEFTITYSAIGID	16
OY	156	-----YADGETLCAPYDFRGLAAEGHPQSOGSK--FLDKL-----	19
Db	167	LASHGTVAATEHRDGSA-SATYYFKQGSAAE-----IGNKSMSTYLOELKPGEDEIHVR	21
OY	192	-----NLI-----EASNSNNGKPVILLSHSGLGF	21
Db	220	NEOVOKRAKECSOALNTLLDIDHGRIKNVLDEFYDLQSDIDRDKIAYIGHFFGGAT	27
OY	218	VLOLLNRNPMSRKRTKHFIATLSAPWGCAIDEMVTFSGMTGCVLPVDPLLVRRQGSS	27
Db	280	VLOALSED-----QR-RCGIATAHW-----MLPDDAIYSR----	31
OY	278	ESNLMLPNPKIFGPOKRVITTPIRPYSAHDMVFLKDIGEPVEGYPY-----ETRI	32
Db	311	-----IPOPLF-----INSER-----FQPENIKKKAKCYSPDKERM	34
OY	330	LEPLGNIKARPOVPTTCIMGTVGHLERTFYKRGPFDERPELSTYGDSGVNLVSLIAIQ	388
Db	345	ITINGSWHONAFDETFTTGKIVGVIYTL--KGDISNVAD-----LCRKASIAIAFQ	394

RESULT 8
 US-08-485-938A-33
 : Sequence 32, Application US/08485938A
 Patent No. 5847088
 GENERAL INFORMATION:
 APPLICANT: Consens, Lawrence S.
 APPLICANT: Eberhardt, Christine D.
 APPLICANT: Gray, Patrick W.
 APPLICANT: Le Trong, Hai
 APPLICANT: Tjoelker, Larry W.
 APPLICANT: Wilder, Cheryl L.
 TITLE OF INVENTION: Platelet-Activating Factor
 TITLE OF INVENTION: Acetylhydrolase
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,938A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/318,905
 FILING DATE: 06-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/133,803

```

1      FILING DATE: 06-OCT-1993
2
3      ATTORNEY/AGENT INFORMATION:
4
5      NAME: No. 584/088and, Greta E.
6
7      REGISTRATION NUMBER: 35,302
8
9      REFERENCE/DOCKET NUMBER: 27866/32792
10
11     TELECOMMUNICATION INFORMATION:
12
13     TELEPHONE: (312) 474-6300
14
15     TELEFAX: (312) 474-0448
16
17     TELEX: 25-3658
18
19     INFORMATION FOR SEQ ID NO: 32:
20
21     SEQUENCE CHARACTERISTICS:
22
23     LENGTH: 444 amino acids
24
25     TYPE: amino acid
26
27     TOPOLOGY: linear
28
29     MOLECULE TYPE: protein
30
31     US-08-485-938A-32

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Query Match	3.9%	Score 92	DB 2	Length 444
Best Local Similarity	20.5%	Pred. No. 0.58		
Matches 98	Conservative 51	Mismatches 122	Indels 208	Gaps 26

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QY 26 SLTCCG-----SNDDPLIGNG-GNDLEARTQVKSPTFICSWPLIKK 75
   : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 8 ALFCLCSLTIVHPIDMDLNPVAHISSAANKIQLMA-----ASINQSRP---KG 59
   : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 76 NGWFR-----LWEDSSVILAFPTCCFAERMT--LHYHQELD----- 110
   : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 60 NGSVSVGCTDLMFD-----YTKKGFTLRLYPSQEDHSDPLMIPNKEYFGLS 108
   : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 111 -YFNTPGVETVVP--HFGSTNSLXLNRLKHITGYAPLPLVDSLOKIG----- 155
   : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 109 KILGPPWLMGKILSEFSESVTTPANMNSPLR--GGEKYPILVFESHGJAFETIYSAIGID 166
   : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 156 -----YADGELFEGAPYDFRXYGLAEHSPQVSGK--PLKDLK----- 191
   : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 167 LASHGFIYAALHEHDGSA--SATYFKQGSAAE-----IGKMSYIQLKPGDELIHVR 219
   : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 192 -----NL-----EASNSNNGKRPVILLSLGLGF 217
   : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 220 NEOVOKRAKECSQALNLDLIDHGRPIKNVLEDFEVDOLKSDIDRPIAVTIGHSFGAT 279
   : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 218 VLQLLNRNRPMSRKRTKHFHIALSAPMGCAIDEMYTFASGNTLGVPLVPLVHSDQSS 277
   : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 280 VLQALSED-----QRF-RCGIALDA-W-----MLPDDALYSR----- 310
   : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 278 ESNLMLNPRIFGQPKRIVITPIRPSAHDMVDFLDIGFPEGVVP-----ETRI 329
   : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 311 -----IPQPLF-----INSR-----FGPENIKMKKKCYSPDKERKM 344
   : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 330 LPLGNITKAPQVPTICMGTCGVGLTLEFYKKGDFERPELSYDGGGTVNLVSLAQ 388
   : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 345 ITRKSHVQNFADFTTGTGKIVGIIETL--KGQIDSNVAD-----LCKKASLAEQ 394
   : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 9
 US-08-947-965-74
 : Sequence 74, Application US/08947965A
 : Patent No. 6004790
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Dijkhuizen, Lubbert
 : APPLICANT: Dijkstra, Baake
 : APPLICANT: Andersen, Carsten
 : APPLICANT: Osten, Claus von der
 : TITLE OF INVENTION: Cyclicalotodextrin Glucanotransferase
 : FILE OF INVENTION: Variants
 : FILE REFERENCE: 4285_204-US
 : CURRENT APPLICATION NUMBER: US/08/947_965A
 : CURRENT FILING DATE: 1997-10-09
 : EARLIER APPLICATION NUMBER: 0477/95
 : EARLIER FILING DATE: 1995-04-21
 : EARLIER APPLICATION NUMBER: 1173/95
 : EARLIER FILING DATE: 1995-10-17
 : EARLIER APPLICATION NUMBER: 1281/95

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: EARLIER FILING DATE: 1995-11-16
: EARLIER APPLICATION NUMBER: PCT/DK96/00179
: EARLIER FILING DATE: 1996-04-22
: NUMBER OF SEQ ID NOS: 78
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO: 74
: LENGTH: 685
: TYPE: PRT
: ORGNISM: Bacillus licheniformis
: OS-08-947-965-74

```

Query Match	3.9%	Score	90.5	DB	3	Length	685
Best Local Similarity	20.1%	Pred. No.	1.7				
Matches	77	Conservative	40	Mismatches	160	Indels	107
						Gaps	16

```

Qy 68 MYPLIKKKN-----GMFRIMPESSVILAFTQCFMERHTLH-----H 1039
Db 55 WQGLVNRKINDNYFESDLDGVTALM-----ISQVENIFA-----TINSGYTNTAYHGYWARDF 106
Qy 106 QELDDYFNT-----PGVETRYRPHFGSTNSLLYLPRL 137
Db 107 KKTINRYETMTMDPQNLVYTHAKSIRIKIIDPAPNHTSPAMETDTSF--AENGKLYDNGNL 164
Qy 138 KHTGYMAPLVDSLOKLGADGETLFGAPYDFERYGLAEGHPSQVSGSKFLDKLNLEE 197
Db 165 --VGGYTNDTNGYFHHNGGSDSFSTLENGIYKNLYDLADLNLNNHNTIDTYEFKDAIKL---- 218
Qy 198 SNSNNKRVILLSHSLGSLFVLOLLNNRPSMKKFKFKHFLA-----LSAPV--GGAIDE 250
Db 219 -----WLDGVOGIRV-DAVKHMPQGMQKNMSSSIYAHKPVFTFGEMVGLSAPD 267
Qy 251 MYTFASGNTLGPVLVD---PLTVRDEORSSESNLMLPNPKIFGQKPIYTPRIPYSAH 307
Db 268 ADNTDFEASCSMSLLDPREFNSAVANVRDRNTSNMYAL-----DSMLTRTADYDQYN 319
Qy 308 DMVDFLADIGFPEGVYRYEYRILRLPLIGNIKAPQVPITCIMGTGVGLT---ETLLEYKGD 363
Db 320 DQVYFIDN-----HMDRFRKTSAVNNRRLQALAFTLNSRGVPALYFGYEQYLTGNGD 372
Qy 364 FDERPEI- SYGDCGYVNLVLSLA 386
Db 373 PDNRGKMPFSFSKSTPAFNVISKLA 396

```

RESULT 10
US-07-642-002-2
Sequence 2, Application US/07/642002
Patent No. 5268465
GENERAL INFORMATION:
APPLICANT: Bredt, David S.
APPLICANT: Hwang, Paul M.
APPLICANT: Reed, Randall
APPLICANT: Snyder, Solomon H.
TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
Oxide Synthase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,002
FILING DATE: 19910118
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

```

? NAME: Kagan, Sarah A.
? REGISTRATION NUMBER: 32,141
? REFERENCE/DOCKET NUMBER: 1107.033576/
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 296-5500
? TELEFAX: (202) 296-7830
? INFORMATION FOR SEQ. ID NO.: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1429 amino acids
? TYPE: AMINO ACID
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-07-642-002-2

```

Query Match	3.9%	Score 90.5	DB 1	Length 1429
Best Local Similarity	18.5%	Pred. No. 5.7		
Matches 67	Conservative 58	Mismatches 142	Indels 95	Gaps 16

[illegible]

RESULT 11
 US-08-365-486A-13
 Sequence 13 Application US/08365486A
 Patent No. 5634306
 GENERAL INFORMATION:
 APPLICANT: Webster, Keith A.
 APPLICANT: Bishopric, Nanette H.
 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 TITLE OF INVENTION: Therapeutic Constructs
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/365,486A
 FILING DATE: 23-DEC-1994
 CLASSIFICATION: 514


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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-342-13
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Query Match 3.9%; Score 90.5; DB 4; Length 1429;

Best Local Similarity 18.5%; Pred. No. 5.7;

Matches 67; Conservative 58; Mismatches 142; Indels 95; Gaps 16;

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QY 108 LDDYFNTPGVETRPVPHGSGNSLLYLNPRLKHITGYAPRYVDSLOKLGADGETLFGAPY 167
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DB 362 LDQYSS-----IKRFGSKAHM---DRLEEVN---KEIESTYQLKDTLETLYGAKH 407

QY 168 DFRYGLAEG-----HPSQVSKFLDKLKNLIEASNSNGKRPVI-LLSHSLG 214
    :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 408 AMRNASRCVGRIQMSKQVDPARDCTTAHGMFNYICHNVKATNKGKLSAIIIFPQRTD 467

QY 215 GLEVLQLLNRPSPWRKKFKHFIALSAPWGAIIDEMTTASGNTLGAPL---VDPILVR 271
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 468 GKHDFFV-----WNSQLIRY-----AGYKQPDGSTLGDPRANVOFTETLCIQ 507

QY 272 DEORSSSENMLLP-----NPKIRG-PQKPIVITPIRPYSAHMWDFLKDIGPPEGV 322
    :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 508 QGKMAPRGPRDVLPRLLQANGNDPELFQIRPELVLEVPPIR---HPRFDMFKDLGLKMWG 563

QY 323 YPETRILPLIGNIKARQVPIIT-CIMGTGVTLETFLFYGKDPDERPEISGDDGTIVNL 381
    :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 564 LPAVSNMLLEIGLEFACPSFGWMTETIGVRD-----YCD-NSKRYNI 606

QY 382 VSLA-----LOSIMKEEKNOYLKVDGVSHTSLKDEVALNEIVGETTSINSH 432
    :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 607 LEEVAKKMDLMKRTSSLMKDO-----ALVEINIAVLVSFQSDKVTIVDHSAATESFIKH 661

QY 433 AE 434
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DB 662 ME 663
```

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RESULT 14
US-08-705-625-4
; Sequence 4, Application US/08705625
; Patent No. 5908756
; GENERAL INFORMATION:
; APPLICANT: Snyder, Solomon H.
; APPLICANT: Jaffrey, Samle R.
; TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
; TITLE OF INVENTION: Oxide Synthase
```

```
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,625
FILING DATE: 30-AUG-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.57071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9299
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-705-625-4
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Query Match 3.9%; Score 90.5; DB 2; Length 1430;

Best Local Similarity 18.5%; Pred. No. 5.7;

Matches 67; Conservative 58; Mismatches 142; Indels 95; Gaps 16;

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QY 108 LDDYFNTPGVETRPVPHGSGNSLLYLNPRLKHITGYAPRYVDSLOKLGADGETLFGAPY 167
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 362 LDQYSS-----IKRFGSKAHM---DRLEEVN---KEIESTYQLKDTLETLYGAKH 407

QY 168 DFRYGLAEG-----HPSQVSKFLDKLKNLIEASNSNGKRPVI-LLSHSLG 214
    :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 408 AMRNASRCVGRIQMSKQVDPARDCTTAHGMFNYICHNVKATNKGKLSAIIIFPQRTD 467

QY 215 GLEVLQLLNRPSPWRKKFKHFIALSAPWGAIIDEMTTASGNTLGAPL---VDPILVR 271
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 468 GKHDFFV-----WNSQLIRY-----AGYKQPDGSTLGDPRANVOFTETLCIQ 507

QY 272 DEORSSSENMLLP-----NPKIRG-PQKPIVITPIRPYSAHMWDFLKDIGPPEGV 322
    :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 508 QGKMAPRGPRDVLPRLLQANGNDPELFQIRPELVLEVPPIR---HPRFDMFKDLGLKMWG 563

QY 323 YPETRILPLIGNIKARQVPIIT-CIMGTGVTLETFLFYGKDPDERPEISGDDGTIVNL 381
    :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 564 LPAVSNMLLEIGLEFACPSFGWMTETIGVRD-----YCD-NSKRYNI 606

QY 382 VSLA-----LOSIMKEEKNOYLKVDGVSHTSLKDEVALNEIVGETTSINSH 432
    :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 607 LEEVAKKMDLMKRTSSLMKDO-----ALVEINIAVLVSFQSDKVTIVDHSAATESFIKH 661

QY 433 AE 434
    :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 662 ME 663
```

```
RESULT 15
US-09-010-998-5
; Sequence 5, Application US/09010998
; Patent No. 6103872
; GENERAL INFORMATION:
; APPLICANT: Snyder, Solomon
```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2003, 19:15:26 ; Search time 30 seconds
(without alignments)
377.272 Million cell updates/sec

Title: US-09-857-612A-14
Perfect score: 2333
Sequence: 1 MKKEQEGELKIEVATLTFTV.....GEITSINSHAEIGLSNLFSG 443

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEM_PUB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCr_NEM_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEM_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEM_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/PCrUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09_NEM_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubppaa/US10_NEM_PUB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US60_NEM_PUB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	610	26.1	412	9	US-09-978-295A-157
2	610	26.1	412	9	US-09-978-697-157
3	610	26.1	412	9	US-09-978-192A-157
4	610	26.1	412	9	US-09-999-812A-157
5	610	26.1	412	9	US-10-001-054-8
6	610	26.1	412	9	US-09-978-189-157
7	541	23.2	440	10	US-09-919-497-80
8	112	4.8	300	9	US-09-738-626-3594
9	106.5	4.6	314	10	US-09-950-368-17
10	103.5	4.4	338	9	US-09-738-626-5970
11	101.5	4.4	574	10	US-09-748-739A-22
12	100.5	4.3	346	10	US-09-896-578-2
13	97.5	4.2	346	10	US-10-027-805-34
14	97.5	4.2	346	10	US-09-903-410-34
15	97.5	4.2	1014	9	US-09-738-626-4656
16	97	4.2	338	9	US-09-738-626-5692
17	95.5	4.1	3169	9	US-10-114-170-257
18	91	3.9	389	10	US-09-815-242-10411
19	90.5	3.9	574	10	US-09-748-739A-6

20	89.5	3.8	416	10	US-09-731-231A-6	Sequence 6, App1
21	89.5	3.8	618	9	US-09-738-626-5766	Sequence 5766, Ap
22	89.5	3.8	7968	9	US-10-077-110-5	Sequence 5, App1
23	89	3.8	350	10	US-09-815-242-5749	Sequence 5749, Ap
24	89	3.8	350	10	US-09-815-242-12468	Sequence 12468, A
25	89	3.8	829	10	US-09-801-368-324	Sequence 324, App1
26	87.5	3.7	333	10	US-09-794-715A-16	Sequence 16, App1
27	87	3.7	233	9	US-10-056-744B-4	Sequence 4, App1
28	87	3.7	251	9	US-10-068-134-4	Sequence 4, App1
29	87	3.7	501	10	US-09-878-262B-1	Sequence 1, App1
30	87	3.7	624	9	US-10-231-353-24	Sequence 24, App1
31	86.5	3.7	574	10	US-09-748-739A-4	Sequence 4, App1
32	86.5	3.7	574	10	US-09-748-739A-8	Sequence 8, App1
33	86.5	3.7	574	10	US-09-748-739A-17	Sequence 17, App1
34	86.5	3.7	574	10	US-09-748-739A-19	Sequence 19, App1
35	86.5	3.7	574	10	US-09-748-739A-20	Sequence 20, App1
36	86.5	3.7	602	10	US-09-748-739A-2	Sequence 2, App1
37	84.5	3.6	811	9	US-09-738-626-5817	Sequence 5817, Ap
38	84	3.6	574	10	US-09-748-739A-18	Sequence 18, App1
39	83.5	3.6	811	10	US-09-895-382-32	Sequence 32, App1
40	83.5	3.6	1399	10	US-09-815-242-5179	Sequence 5179, Ap
41	83.5	3.6	1610	9	US-09-738-626-6666	Sequence 6666, Ap
42	83	3.6	322	9	US-09-738-626-3508	Sequence 3508, Ap
43	83	3.6	477	9	US-10-047-412A-10	Sequence 10, App1
44	83	3.6	477	10	US-09-923-556-6	Sequence 6, App1
45	83	3.6	477	10	US-09-987-025-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-09-978-295A-157
; Sequence 157, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978, 295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          26.1%; Score 610; DB 9; Length 412;
Best Local Similarity 34.8%; Pred. No. 2e-49;
Matches 141; Conservative 80; Mismatches 156; Indels 28; Gaps 12;

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QY 137 LKHTTGMAPLVDSLQKLGADSETLFGADYDFRYGLAAGHPSQVGSFKLKNLIEE 196
DB 131 KSSVGSYFHMVSESLVGMGTGCEDEVGAPYDWRA-----PNENGPYLA-LREMIIE 183
QY 197 ASSSNNKGPVILSHSLGCLFVQLNRRNPSSRKKFKIKHILMSAPMGAIEMTFAS 256
DB 184 MYQLYGG-PVVLVAHSMGNNTYTLFQROQAWKDYIRAFVSLGAPWGVAATLRYLAS 242
QY 257 GNTLYGVLVDLIVRDEORSSESMLLNPKEFGPKPIVPIPIPPYSAHDWVFLKDI 316
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QY 317 GPPEG-VPEYETRIPLIGNIKAPQVPTICMGTVGTTLEFLYGGDFDER-PEISYGD 374
DB 303 GFEDGMLMRDTE--GLVEATMPPGVQLHCLYGTGVTPSPFY--ESFPDRPKICFGD 358
QY 375 GDSVTMLVSLALOSLMKEKNQYLVKVKIDGVSHTSILKDEVAL 419
DB 359 GDSVTMLKSLQCOA-WOSRQHOVILLQELPGESEHTEMNATTL 402

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; APPLICANT: Pan, James;
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; TITLE OF INVENTION: Acids Encoding the Same
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;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 26.1%; Score 610; DB 9; Length 412;

Best Local Similarity 34.8%; Pred. No. 2e-49; Matches 141; Conservative 80; Mismatches 156; Indels 28; Gaps 12;

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Qy 137 LKHITGYAPLVDLSQKGYADGETLFCAPYDFRYGLAEGHPSQVSKFLDKNLIEE 196
Db 131 KSSVGSYHTHWESLVGKTYRGEDEVKAPYDWRRA-----PDENGFFLA-LREKIEE 183
Qy 197 ASNSNNGKPVILLSHSLGLEFVLQNLNPPSWRKKFKHFIASAPWGAIDEMYTFAS 256
Db 184 MYQLXGG--PVVLVAHSMKNMTYFELQRPQAMKDKYIRAVVSLGAPGVAKTLRYLAS 242
Qy 257 GNTLGVPLVLDLVNDEGRSSSNMILLPNPKIEGPKPIYITPIRPSAHDMVDFLKI 316
Db 243 GDMNRIPVIGPLKIREQORSVSTSMILPYNYVTSPEKVFQPTINTLTDYKRFQDI 302
Qy 317 GPFGS--VYVYETRIPLPLGNKAKQVPTICIMGCGVGLLEFLYKGDGFDER--PEISYGD 374
Db 303 GFEDGMLRQDTE--GLVEATMPRGVQHCXYGCVLPDPSFY--ESFPDRDKICFGD 358
Qy 375 GDGTYNLVSLALQSLMKKEKNQYLKVKIDGVSTSLIKREVAL 419
Db 359 GDGTYNLKSALQCA--WOSROHOVLQDELPGSEHIEMLNATTL 402

RESULT 3

US-09-978-192A-157

Sequence 157, Application US/09978192A

Patent No. US20020177553A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630Plc9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

```

Query Match 26.1%; Score 610; DB 9; Length 412;

Best Local Similarity 34.8%; Pred. No. 2e-49;

Matches 141; Conservative 80; Mismatches 156; Indels 28; Gaps 12;

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QY 21 VVVMLSLDC--TCGASNDPLLLIPGNGQLARLTNOYKPT--FICSMYPLIKKN 76
DB 20 LLLLLLMDPALPACRHPBPVVLVPGDLGQLEAKLD---KPTVYVLS-----KTE 70
QY 77 GWERLWDSVILAPFTQCAERMTLHYHQLDVFNTPCVETRVVPHFGTSLXLNPR 136
DB 71 SYFTILNLELLPVIIIDMIDNIRLVYKNTSRATQPPGCVDRVYVGFGTSELEFLDS 130
QY 137 LKHTTGYMAPLVDSLOKLGADSETLFGAPYDERYLAAEGHPSQVSKFLDKNLIEE 196
DB 131 KSSVGSYFTHTWESLVGMCYTRCEDVRGAPYDWRRA-----PNEGPFYFLA-LREITEE 183
QY 197 ASSNSNNGKPIIILSHSLGFLVQQLNRNPPSRKKFIKHFTLSAPKSGAIDEMTFKS 256
DB 184 MWOLYGG-PVVLVAHSMGNNYTLTYLQROPQAKWXYIRAFVSLGAPWGVANTLRLVLS 242
QY 257 GNTLGVLPVLPVLRDEQSSSESNLMLLPNKIFGQKPIVIRIPYSAHMDVDFLKI 316
DB 243 GDNRRPVPVIGPLKIRGOQSAVSTSWLLPYNTYMSFEKVFVQPTINTYLRDRKRFDDI 302

```

```

QY 317 GFPEG-VYPYETRIPLIGNIKAPOVPTICMGVGTLETFYKGFDPDER-PEISYGD 374
DB 303 GFEDGMRLQDTE--GLVEATMPPGVGLHCLYGVPTPDSFY--ESFPDRPKICFGD 358
QY 375 GDGTVNLVSLLAQSLMKEEKNOYKAKIDGVSHTSLKDEVAL 419
DB 359 GDGTVNLKSAIQQA-WQSRQHOVLQLPGLGSEHTEMLNATVL 402

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RESULT 4

US-09-999-832A-157

Sequence 157, Application US/09999832A

Publication No. US20020192706A1

GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999, 832A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/07450
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; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910

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; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 8
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-8

Query Match      26.1%; Score 610; DB 9; Length 412;
Best Local Similarity 34.8%; Pred. No. 2e-49;
Matches 141; Conservative 80; Mismatches 156; Indels 28; Gaps 12;

QY   21 VVWMSILC--TCGSNNDPLILIPGNGGNLEARLTNQYRPT--FCCESMYPLIKKN 76
    20 LLLMLLADPALPRGRHPPVLPVGDLGNOLEAKLD---KPYVHYICS-----KTE 70
Db    77 GWFLMPSDSVYLAPFTOCFAERMWLHAHOELDDYFNTPGVETRYPHFSNSLLYNLR 136
    71 SYFTFWNLBELLPRIIDCMWDINRLYYNKSRATQFPDGDVARYRGKGKFFSLEFDPS 130
QY   137 LKHITGWAPLVDSIQKLGVADGETLEGAPYDFRYGLAEBGPSOVSGSKFLDKLNLEE 196
    131 KSSVGSYHTFWESTIVSGCTRGEDVRGAPYDWRRRA-----PNENGPFILA-LREMLEE 183
Db    197 ASNSNGKPVLILLSLGGLFYQLNNPSPWRKKFIKHFIALSAPMGALIDEYTTAS 256
    184 MYOLYG-PVVVALHASMNMNYTLFLORPOAMKDXYIRAFVSLGAPWGVAKTLYLAS 242
QY   257 GNTLGVPVLVDLLVDEBGRSESNNMLLPNPKIFGPQKIYTPTRPYSAHDMDVFLDI 316
    243 GDNNRPIPIGPKLRHQORSAYSTSWLPIYNTWSPEKVYPQTPIINTLTDRKRFODI 302
QY   317 GFPEG-VYPEYETRILLIGNIKAPOVPTICMGTVGTLETLEYKGDGEDER-PEISYGD 374
    303 GFEDWMLRPDTE--GLVEATMPPEVQLCHLCXGTGVTPTDPSPY--ESFPDRDPCRPD 358
QY   375 GDGYTNLVSLLAGLSMKEEKNQYLKYVKIKDGVSHTSLKDEVAL 419
    359 GDGYTNLKSLAQCA-WQSROEHVLLDELPGSEHIEMLANATT 402

RESULT 6
US-09-978-189-157
; Sequence 157, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

```

;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2630PIC7
;; CURRENT APPLICATION NUMBER: US/09/978,189
;; CURRENT FILING DATE: 2001-10-15
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
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;; PRIOR APPLICATION NUMBER: 60/066364
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;; PRIOR APPLICATION NUMBER: 60/077649
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;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07

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; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
;
Query Match
Best Local Similarity 34.8%; Score 610; DB 9; Length 412;
Matches 141; Conservative 80; Mismatches 156; Indels 28; Gaps 12;
```

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Qy 21 VVWMLSLC--TCGASNDPILILPGNGNQLARLTNQKRSST--FICESWYPLIKKRN 76
    ::::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 20 LLLLLMLADPALPAGRHPPVLPVPGDLGNQLEAKID--KPTVVHYLCS-----KKEE 70
Qy 77 GWFRLMFPSSVTLAFTQCFARMTLHYHQLDLYFNTPGVETVRPHGSGNSTSLYLNR 136
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 SYFTIMLMLLELLPYIICWIDINIRLVYKNSRATQFPDGVAVRVPGEKTFESLEFLDS 130
Qy 137 LKHITGYAPRLVDSLOKGYADGETLFGAPYDFRYGLAEGHPSQVSGSKFLDKNLIEE 196
    : : : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131 KSSVGSYHTHWESLWKGCTYRGEIVRGAPYDMRA-----PNEGPFYLA-LKEMIE 183
Qy 197 ASNSNGRPVILLSHSLGFLVQLINRNPSPMRKRFIKHFTALSPAGCAIDEMYTEAS 256
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 184 MYQLVGG--PVVLVANSMGWMTLYFLQRPQAMKDKYITAFSLGAPMGVAKTLRYLAS 242
Qy 257 GNTLCVPLVDPLVDEORSSSNMLLPNKIFGPQKPIVTPPIRPSAHMDVDFLNDI 316
    : : : : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 243 GDNMRIPVIIGPLKIREQORSASTSMLLPNYTMSPEKVFQPTPIINYLRIRKFFODI 302
Qy 317 GPPES--VYPERIRLPLIGNIKAPQVPITCIMGVGTLETLFYGKGDDER--PEISYGD 374
    | | : : : : | | : : : : | | | | | | | | | | | | | | | | | |
Db 303 GFEDGWLKRQDTE--GLVEATMPPGVQHLCLGTGVPPDSFY--ESFPDRDPKICFSD 358
Qy 375 GGGTVNLVSLALQSLMKEEKNOYLKVVKIDGVSHTSIKDEVAL 419
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 359 GDGTVNLKSLAQCGA--WQSRQEHQVLLQELPSEHIEMLANNTTL 402
```

```

RESULT 7
US-09-919-497-80
; Sequence 80, Application US/09919497
; Patent No. US2002010662A1
; GENERAL INFORMATION:
; APPLICANT: Muller, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT FILING DATE: 2001-07-31
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patent version 3.0
; SEQ ID NO 80
; LENGTH: 440
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```

; TYPE: prf
; ORGANISM: Homo sapiens
US-09-919-497-80
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```

Query Match
Best Local Similarity 23.2%; Score 541; DB 10; Length 440;
Matches 129; Conservative 74; Mismatches 162; Indels 22; Gaps 11;
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Qy 38 PLILPGNGNQLARLTNQKRSSTFICESWYPLIKKNGWFLMDFSSVILAPFTQCF 97
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 48 PYLVPGCLGNQLEAKID--KPDVV---NM-CYKRTDEFTIWMILMFLPLGVDCWI 100
Qy 98 EMTLHYHQLDLYFNTPGVETVRPHGSGNSTSLYLNPRLKHTGYMAPLNSLOKLYA 157
    : : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 101 DNTRVVYNNSSGLVSNAPQIRVPGFGKTVSEYIDS--SKLAGLHTLVQLVNNGTV 158
Qy 158 DDETLFGAPYDFRYGLAEGHPSQVSKFLDKNLIEEASNSNNKPYILLSHSLGFL 217
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 RDETVAAPIYDRL-----EPGQ-QEYRYKLAGLVE--MHAAYKPFVLGHSIGCLH 210
Qy 218 VQLLNRPSPMRKRFIKHFTALSPAGCAIDEMYTEFASGNTLVPLVDPLVDEORSS 277
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 211 LLYFLRQPOAMKDRIFDFTISLGAPMGGSIKPMLYLASGDNQGIPIMSIKLKEORIT 270
Qy 278 ESNMLLPNKIFGPQKPIVTPPIRPSAHMDVDFLKDIFGPGVVPY--ETRLPLIGNI 336
    : : : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 271 TTSPPMFPSPRMAMPEDHVEISTPSEFNVTGRDQRFADLFEFGWYMWLQSR--DLLAGL 328
Qy 337 KAPQVITCIMGVGTLETLFYGKG--DDEPEREISYGDDGVTVNLSLALQSLMKEEK 395
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 329 PARGVETLYGVGLFPTPTIYDHGFPTTDPVGVLYEDGDITVATRS--TELQGLMQGRQ 387
Qy 396 NOYLKVVKIDGVSHTSIKDEVALNEI 422
    : : : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 388 PQVHLLPLHGIQHLNMFPSNLLEHI 414
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RESULT 8
US-09-738-626-3594
; Sequence 3594, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent ver. 3.0
; SEQ ID NO 3594
; LENGTH: 300
; TYPE: prf
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3594
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Query Match
Best Local Similarity 4.8%; Score 112; DB 9; Length 300;
Matches 76; Conservative 53; Mismatches 107; Indels 142; Gaps 21;
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QY 96 FAERMTLHYHOELDDYFNTPGVETRVPHFGSTNSLLYLNPRLKHITGYMA----- 145
||| | ||| | : || | ||| | :
Db 28 FAERT-----QELVDH-----ATNITLPLTALKP-KGFFQODMRARPSGA 68
QY 146 ---PLV-----DSLQKLG---YADGETLFGAPYDFRYGLAEGHPSOVSGKFLKOL 190
||| | ||| | : ||| | :
Db 69 RPPVIVLHSGASKSGSWEEMGAELRSKMVAFAPDECTRAPIAASAOIGAYI--DA 126
QY 191 KNLLEASNSNNGKPVILLSHSISGLFVLQLLNNRPPSMRKKF-----IKHPIALASAP-- 243
||| | ||| | : ||| | :
Db 127 VLVYGAAG-----IVLVHSGGVARY-----WMPTVGGYMKVRHMISTEPNH 172
QY 244 ---MGAIIDEMYTRASGNTLGPVLDPLLVDEQRSSESIMLLPNPKIFGPOKEVITP 300
||| | ||| | : ||| | :
Db 173 GTLGGILNPMTKYKSGE---GTIEKLMHR-----LFGP-----TG 205
QY 301 IRPISAHDMVPLKDIGPPEGVYPERILPLIGNIKAPQVPTICMGTCVGTLETFYG 360
||| | ||| | : ||| | :
Db 206 FEOLRGHDIIEFLAD-----GDDLDPGVYTCI-GTHF----- 237
QY 361 KGDEDEREISY--GDGDGVNLVSLALQSLMKKEKNQYKVKIDGVSHTSILKDEVA 418
||| | ||| | : ||| | :
Db 238 -DPTIQPEVAFLEVNEDDPRRY-----HNIVDEHPRAM-----IAHNDVDRPV 285
QY 419 LNEIVGEITSINSHAEIG 436
||| | ||| | : ||| | :
Db 286 IEIVRAELDRY---ARLG 300

RESULT 9
US-09-950-368-17
; Sequence 17, Application US/09950368
; Patent No. US20020061580A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GC511-PCR
; CURRENT APPLICATION NUMBER: US/09/950,368
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/355,166
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Bacillus
US-09-950-368-17

Query Match 4.6%; Score 106.5; DB 10; Length 314;
Best Local Similarity 21.9%; Pred. No. 0.03;
Matches 65; Conservative 34; Mismatches 109; Indels 89; Gaps 12;
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RESULT 10
US-09-738-626-5970
; Sequence 5970, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5970
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5970

Query Match 4.4%; Score 103.5; DB 9; Length 338;
Best Local Similarity 20.7%; Pred. No. 0.063;
Matches 72; Conservative 47; Mismatches 119; Indels 109; Gaps 16;
```


LENGTH: 346 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-027-805-34

Query Match 4.2%; Score 97.5; DB 9; Length 346;
Best Local Similarity 25.1%; Pred. No. 0.24;
Matches 42; Conservative 24; Mismatches 64; Indels 37; Gaps 8;

QY 143 YNAPLVDSLOKGYADGETLFGAPYDFRGLAEGHPSQVSKFLDKNLLEASNSNN 202
DB 142 YNAPVLARELVEWGYR-----VVVFDFR-GHGESGSGTTIGPREVLDAVAVGYVSERFP 194
QY 203 GKPVILLSLGLFLV-----QLNRPSPMR-KKFIKHFALSAP---MGCATD 249
DB 195 GKRIILVGSKMGAAVAIVGAGDPRVYAAADSPYIRLDVIRPMLEYKTPPLPGWGYLA 254
QY 250 EMY-TFASGNTLGV-----PLV-----DPLLVRDEQRSSSES 279
DB 255 GFYGRMLAGVDLGFPGAGYGRVDKPLLVYGYPRDPLVTDEARSLAS 301

RESULT 14
US-09-903-410-34
Sequence 34, Application US/09903410
Patent No. US20020146799A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: ROBERTSON, Dan
APPLICANT: MURPHY, Dennis
APPLICANT: REID, John
APPLICANT: MAFFIA, Anthony
APPLICANT: LINK, Steven
APPLICANT: SWANSON, Ronald
APPLICANT: WARREN, Patrick
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: DIVER1180-2
CURRENT APPLICATION NUMBER: US/09/903,410
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/382,242
PRIOR FILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: US 08/602,359
PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 346
TYPE: PRT
ORGANISM: Pyrodicticum
US-09-903-410-34

Query Match 4.2%; Score 97.5; DB 10; Length 346;
Best Local Similarity 25.1%; Pred. No. 0.24;
Matches 42; Conservative 24; Mismatches 64; Indels 37; Gaps 8;

QY 143 YNAPLVDSLOKGYADGETLFGAPYDFRGLAEGHPSQVSKFLDKNLLEASNSNN 202
DB 142 YNAPVLARELVEWGYR-----VVVFDFR-GHGESGSGTTIGPREVLDAVAVGYVSERFP 194
QY 203 GKPVILLSLGLFLV-----QLNRPSPMR-KKFIKHFALSAP---MGCATD 249
DB 195 GKRIILVGSKMGAAVAIVGAGDPRVYAAADSPYIRLDVIRPMLEYKTPPLPGWGYLA 254
QY 250 EMY-TFASGNTLGV-----PLV-----DPLLVRDEQRSSSES 279
DB 255 GFYGRMLAGVDLGFPGAGYGRVDKPLLVYGYPRDPLVTDEARSLAS 301

RESULT 15
US-09-738-626-4656

Sequence 4656, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4656
LENGTH: 1014
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4656

Query Match 4.2%; Score 97.5; DB 9; Length 1014;
Best Local Similarity 22.9%; Pred. No. 1.1;
Matches 79; Conservative 36; Mismatches 109; Indels 121; Gaps 19;

QY 150 SLQKGYADGETLFGAPYDFR-----YGLAEGHPSQVSKFLK--DLKNLIEASN 199
DB 370 SMPKIQNIDGE-----PMDEKESPSMALRGQGVGLAKLGEVLGEDPDLARRIFEISA 424
QY 200 SNNKRPVILLSLGLFLVLOLNNNPSPMRKKFIKHFALSAPGCATDEMYT----- 253
DB 425 S-----PMYLRGETPG-----HALVT--WHDSTNEYTMOQLTL 457
QY 254 -FASGNTL-----GVPLVDPPLVRDEQRSSSESNLMLPNPKIFGPOKPIYTPIRPYSA 306
DB 458 AVEESRLFEKAPQGIAMD-----SGE-----IWMANSFQDL--VCTTPYRLRGL 503
QY 307 HDMPDLKDIGFPEGVYPIETRIIL-----PLGINIRAPQVPIITCINGTGVG 352
DB 504 N-----LEDGVEEGTMEYVTEVLSDPEAVVHLDRSLFTLRGKQKNVAMSFSS--MGNVGG 557
QY 353 TLETLFYCGDPERPEI-----SYGDGCVTVNLVSLALOS-----LWKKEKN----- 396
DB 558 RIETLLVNVVDVTERQELIEVLEHLADHDSLTGLVNRRLRLESDIELLIKKNERDSTDSAL 617
QY 397 -----QYLKVVKIDGVSH-----TSILKDEVALNEIYGEI 426
DB 618 LLLDLDFREVN-DSLGHAGDQLLIEFAELLKDSVRSDDIVGRI 661

Search completed: February 11, 2003, 19:20:22
Job time : 32 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 19:13:15 ; Search time 21 Seconds
(without alignments)
2027.979 Million cell updates/sec

Title: US-09-857-612A-14
Perfect score: 2333
Sequence: 1 MKKEQEGKLEVALTVTV.....GEITSINSHALGSLNLEFSG 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR-73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	23.2	440	1 XXHUN	phosphatidylcholin
2	537	23.0	440	2 JC1502	phosphatidylcholin
3	516	22.1	438	1 XXMSN	phosphatidylcholin
4	515	22.1	413	2 I50662	lecithin-cholester
5	515	22.1	440	1 XXRTN	phosphatidylcholin
6	512.5	22.0	417	2 T23726	hypothetical prote
7	457.5	19.6	272	2 T41755	hypothetical prote
8	181	7.8	623	2 T40685	phosphatidylcholin
9	163	7.0	665	2 T51780	hypothetical prote
10	147	6.3	552	2 C86171	hypothetical prote
11	125.5	5.4	493	2 T04767	hypothetical prote
12	113	4.8	600	2 E86854	hypothetical prote
13	109	4.7	984	2 T44608	pyruvate carboxyla
14	106.5	4.6	314	2 B70013	hypothetical prote
15	106	4.5	586	1 S73355	exonuclease ABC c
16	105.5	4.5	529	2 AD1042	hypothetical prote
17	105	4.5	757	2 T38124	hypothetical prote
18	104	4.5	317	2 T00550	probable phospholi
19	102	4.4	249	2 H87675	hydroxylase, alpha/b
20	102	4.4	542	2 JN0438	carboxylesterase (
21	101.5	4.4	1407	2 T28702	probable polyketid
22	101	4.3	771	2 T47071	hypothetical prote
23	99.5	4.3	434	2 AD0014	hypothetical prote
24	99.5	4.3	732	2 AD0014	primosomal protein
25	99	4.2	605	2 F35216	FRP6 protein - fow
26	98.5	4.2	830	2 T07824	1,4-alpha-glucan b
27	98.5	4.2	1626	2 T09271	probable tail comp
28	98	4.2	989	2 S69711	hypothetical prote
29	97.5	4.2	390	2 T48524	lysophospholipase-

ALIGNMENTS

30	97.5	4.2	861	1 S34730	1,4-alpha-glucan b
31	96.5	4.1	331	1 A70032	conserved hypothet
32	96	4.1	631	2 AH0317	penicillin-binding
33	95.5	4.1	286	2 D75217	probable 2-acetyl-
34	95.5	4.1	3169	2 T00296	toxin B - Escheric
35	95	4.1	297	2 C83311	hypothetical prote
36	95	4.1	357	2 D69820	hypothetical prote
37	95	4.1	446	2 H97091	chitinase family p
38	94.5	4.1	476	2 F81340	glutamate-ammonia
39	94.5	4.1	1137	2 E86708	pyruvate carboxyla
40	94	4.0	462	2 T01732	urp-glucose glucos
41	94	4.0	1019	2 C96519	probable disease r
42	93.5	4.0	209	2 B82501	hypothetical prote
43	93.5	4.0	1269	2 A90267	proteinasase relat
44	93	4.0	373	2 F72602	probable acetylpol
45	93	4.0	417	1 TVCRGC	phosphoglycerate k

RESULT 1
XXHUN
phosphatidylcholine-sterol O-acetyltransferase (EC 2.3.1.43) precursor [validated] - hu
N:Alternate names: lecithin-cholesterol acyltransferase precursor; phospholipid-chole
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Jun-2002
C:Accession: A00571; A25575; A29661; J00036; A29133; I52260; A28511
R:McLean, J.; Fielding, C.; Drayna, D.; Dieplinger, H.; Baer, B.; Kohr, W.; Henzel, W
Proc. Natl. Acad. Sci. U.S.A. 83, 2335-2339, 1986
A>Title: Cloning and expression of human lecithin-cholesterol acyltransferase cDNA.
A:Reference number: A00571; MUID:86205550; PMID:3458198
A:Accession: A00571
A:Molecule type: mRNA
A:Residues: 1-440 <MCL1>
A:Cross-references: GB:M12625; NID:9187022; PIDN:AAA59498.1; PID:9307117
R:McLean, J.; Wion, K.; Drayna, D.; Fielding, C.; Lawn, R.
Nucleic Acids Res. 14, 9397-9406, 1986
A>Title: Human lecithin-cholesterol acyltransferase gene: complete gene sequence and
A:Reference number: A25575; MUID:87091568; PMID:3797244
A:Accession: A25575
A:Molecule type: DNA
A:Residues: 1-440 <MC12>
A:Cross-references: GB:X04981; NID:934286; PIDN:CMA28651.1; PID:934287
R:Rogne, S.; Skretting, G.; Larsen, F.; Myklebost, O.; Mewag, B.; Carlson, L.A.; Holm
Biochem. Biophys. Res. Commun. 148, 161-169, 1987
A>Title: The isolation and characterisation of a cDNA clone for human lecithin:choles
A:Reference number: A29661; MUID:88049652; PMID:2823801
A:Accession: A29661
A:Molecule type: mRNA
A:Residues: 13-440 <RCG>
A:Cross-references: GB:M17959; NID:9187026; PIDN:AAA59500.1; PID:9386858
R:Tata, F.; Chaves, M.E.; Markham, A.F.; Scrace, G.D.; Waterfield, M.D.; McIntyre, N.
Biochem. Biophys. Acta 910, 142-148, 1987
A>Title: The isolation and characterisation of cDNA and genomic clones for human leci
A:Reference number: A90666; MUID:88050546; PMID:2823898
A:Accession: J00036
A:Molecule type: mRNA
A:Residues: 17-256, 'H', 258-440 <TAT>
A:Cross-references: GB:X06537; NID:934284; GB:M26268; NID:9187024; PIDN:AAA59499.1; P
A>Note: the authors translated the codon CAT for residue 241 as ile and CAG for resid
R:Yang, C.; Manojan, D.; Peo, O.; Lee, F.; Knapp, R.D.; Gotto Jr., A.M.; Pownall, H
J. Biol. Chem. 262, 3086-3091, 1987
A>Title: Lecithin: cholesterol acyltransferase. Functional regions and a structural m
A:Reference number: A29133; MUID:87137578; PMID:2880847
A:Accession: A29133
A:Molecule type: protein
A:Residues: 25-284, 'Q', 286-333, 'Q', 335-440 <YAN>
R:Buyo, H.; Kusunoki, J.; Ogasawara, M.; Yamamoto, T.; Ohta, Y.; Shimada, T.; Saito,
Biochem. Biophys. Res. Commun. 181, 933-940, 1991
A>Title: Molecular defect in familial lecithin:cholesterol acyltransferase (LCAT) def
A:Reference number: I52260; MUID:92109783; PMID:1662503
A:Accession: I52260

F:25-438/Product: phosphatidylcholine-sterol acyltransferase #status predicted <MAT>
F:44,108,296,408/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.1%; Score 516; DB 1; Length 438;
Best Local Similarity 33.0%; Pred. No. 2,1e-33;
Matches 128; Conservative 72; Mismatches 164; Indels 24; Gaps 12;

QY 38 PLLIPGNGNGOLEARLTNQYKPSFFICSWYPLIKKNGWRMLMDDSSVILAFPTQCA 97
DB 48 PVLVPGCGGNRLKALD---KPDVY---NMV-CYRKTEDEFTIWDPMFLPLGVDCMT 100
QY 98 ERMATLHYHOELDDYFNTPGVETRVPHFGSTNSLLYLNPRLKHITGYMAPLVDSIQKGYA 157
DB 101 DMTRIYVNNSSGRVSNAPGVQIRVPGFKTSEVEYVD--NKLAGLHLTVQNLVANGYV 158
QY 158 DGETLFGADYDFRYGLAAGHPQSQVSKFLDKLNLIEASNSNNGRPVILLSHSIGLGF 217
DB 159 RDETVRAAPYDWRLA-----PRQ-ODEYXKRLAGLVEE-MYAAVYKRPVLLIGHSIGLCH 210
QY 218 VLQILNRNPPSRMKKFIKHFILSAPWGAIDEMTEFAAGNTLGVPLVDPPLVDRDQRRS 277
DB 211 VHLFLRQPSQWKHFIDGFIISLGAHPWGSIKAMRIASGDNQGIPIILSNIKLKEQRIT 270
QY 278 ESNMLLNPMPKIFGQKPIVITPIRPSAHMDVDFLKDIGFPEGVYVY-ETRIILPLIGNI 336
DB 271 TTSPPMLPAPHVWPEDHVYISTPNFNVTYQDEREFITDLHPEGMHMFQISR--DLLERL 328
QY 337 KAPQVPITCIMGVGTLETFLFYGKGDPEREPEIS--YDGGGTYNVLVSLALQSLMKKE 394
DB 339 PAPGEVYCLVGVGRPTPTTYIDH-NFPYKDPVALYEDGDDYVATRS-TELGGQWGR 386
QY 395 KQOYLKVVKIDGVSHTSILKDEVALMEI 422
DB 387 QSQPYHLPLMNETDHLNMVFSNKTMEHT 414

RESULT 4

150662
lecithin-cholesterol acyltransferase - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C:Accession: 150662
R:Hengstschaeger-Ottstad, E.; Kuchler, K.; Schneider, W. J.
J. Biol. Chem. 270, 26139-26145, 1995
A:Title: Chicken lecithin-cholesterol acyltransferase. Molecular Characterization reveal
A:Reference number: 150662; MUID:96064680; PMID:7592817
A:Accession: 150662
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-413 <HEND>
A:Cross-references: EMBL:X91011; NID:g1050479; PIDN:CAA62493.1; PID:g1050480
C:Superfamily: phosphatidylcholine-sterol acyltransferase

Query Match 22.1%; Score 515; DB 2; Length 413;
Best Local Similarity 31.6%; Pred. No. 2,4e-33;
Matches 121; Conservative 76; Mismatches 166; Indels 20; Gaps 9;

QY 38 PLLIPGNGNGOLEARLTNQYKPSFFICSWYPLIKKNGWRMLMDDSSVILAFPTQCA 97
DB 46 PVLVPGCGGNRLKALD---KPDVY---NMV-CYRKTEDEFTIWDPMFLPLGVDCMT 98
QY 98 ERMATLHYHOELDDYFNTPGVETRVPHFGSTNSLLYLNPRLKHITGYMAPLVDSIQKGYA 157
DB 99 DMTRIYVNNSSGRVSNAPGVQIRVPGFKTSEVEYVD--NKLAGLHLTVQNLVANGYV 156
QY 158 DGETLFGADYDFRYGLAAGHPQSQVSKFLDKLNLIEASNSNNGRPVILLSHSIGLGF 217
DB 157 RDETVRAAPYDWRLA-----PRQ-ODEYXKRLAGLVEE-MYAAVYKRPVLLIGHSIGLCH 210
QY 218 VLQILNRNPPSRMKKFIKHFILSAPWGAIDEMTEFAAGNTLGVPLVDPPLVDRDQRRS 277
DB 209 VLYFLLOQKQAWKQYIGGFISLGAHPWGSVAPLRYLASGDNQGIPIILSNIKLKEQRIT 268

QY 278 ESNMLLNPMPKIFGQKPIVITPIRPSAHMDVDFLKDIGFPEGVYVETRIILPLIGNI 337
DB 269 TTSPPMLPAPHVWPEDHVYISTPNFNVTYQDEREFITDLHPEGMHMFQISR--DLLERL 328
QY 338 APOVPITCIMGVGTLETFLFYGKGDPEREPEISYDGGGTYNVLVSLALQSLMKKEKN 396
DB 328 PGEVDYICLYGTGPTVETRYIDEHPEPDMYIGDGGDYVATRS-TELCKRWNRQK 386

QY 397 QYILKVKIDGVSHTSILKDEVAL 419
DB 387 QKVHVOELRGIDHLNMVFSNLT 409

RESULT 5

XXXXTN
phosphatidylcholine-sterol O-acyltransferase (EC 2.3.1.43) precursor - rat
N:Alternate names: lecithin-cholesterol acyltransferase precursor; phospholipid-chole
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Jun-2002
C:Accession: S11214; S11302
R:Meroni, G.; Margaretti, N.; Magnaghi, P.; Taramelli, R.
Nucleic Acids Res. 18, 5308, 1990
A:Title: Nucleotide sequence of the cDNA for lecithin-cholesterol acyl transferase (L
A:Reference number: S11214; MUID:90384859; PMID:2402469
A:Accession: S11214
A:Molecule type: mRNA
A:Residues: 1-440 <MER>
A:Cross-references: EMBL:X54096
R:Taramelli, R.
submitted to the EMBL Data Library, July 1990
A:Reference number: S11302
A:Accession: S11302
A:Molecule type: mRNA
A:Residues: 1-389, G, 391-440 <TAR>
A:Cross-references: EMBL:X54096; NID:g56563; PIDN:CAA83030.1; PID:g56564
C:Comment: The active enzyme catalyzes the transfer of acyl groups from lecithin to a
cluding cholesterol, can act as acceptor. Apolipoprotein A-I is a potent activator fo
C:Genetics:
A:Gene: LCAT
C:Superfamily: phosphatidylcholine-sterol acyltransferase
C:Keywords: acyltransferase; glycoprotein; lipid metabolism; lipoprotein
F:1-24/Domain: signal sequence #status predicted <SID>
F:25-438/Product: phosphatidylcholine-sterol acyltransferase #status predicted <MAT>
F:44,108,296,408/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.1%; Score 515; DB 1; Length 440;
Best Local Similarity 32.8%; Pred. No. 2,6e-33;
Matches 128; Conservative 75; Mismatches 159; Indels 28; Gaps 12;

QY 38 PLLIPGNGNGOLEARLTNQYKPS--TFICESWYPLIKKNGWRMLMDDSSVILAFPTQ 95
DB 48 PVLVPGCGGNRLKALD---KPNVNMWLC-----YRKTEDEFTIWDPMFLPLGVDC 98
QY 96 FAERMTLHYHOELDDYFNTPGVETRVPHFGSTNSLLYLNPRLKHITGYMAPLVDSIQK 155
DB 99 WIDMTRIYVNNSSGRVSNAPGVQIRVPGFKTSEVEYLD--NKLAGLHLTVQNLVANG 156
QY 156 YADGETLFGADYDFRYGLAAGHPQSQVSKFLDKLNLIEASNSNNGRPVILLSHSIG 215
DB 157 YRDETVRAAPYDWRLA-----PRQ-ODEYXKRLAGLVEE-MYAAVYKRPVLLIGHSIG 208
QY 216 LFLVQILNRNPPSRMKKFIKHFILSAPWGAIDEMTEFAAGNTLGVPLVDPPLVDRD 275
DB 209 LNVHLFLRQPSQWKHFIDGFIISLGAHPWGSIKAMRIASGDNQGIPIILSNIKLKE 268
QY 276 SSESNNMLLNPMPKIFGQKPIVITPIRPSAHMDVDFLKDIGFPEGVYVY-ETRIILPLIG 334
DB 269 ITTSPWMLPAPHVWPEDHVYISTPNFNVTYQDEREFITDLHPEGMHMFQISR--DLA 326
QY 335 NIKAPQVPITCIMGVGTLETFLFYGKGDPEREPEIS--YDGGGTYNVLVSLALQSLMK 392
DB 327 GLPAPGEVYCLVGVGMPTPAHTYTYIDH-NFPYKDPVALYEDGDDYVATRS-TELGGOV 384

294 KPIVITPIRPYSAHMDVFLDKI-----GFPEGVYETREIL-----P 331
408 RRDIDKDHDFIDALQFLKAVTFDDPKVMYAKMYSHGLATEKEVYLNKNNPSPKNTMP 467
332 LIGNIK-APQVPTICMGTGVTLETFYKGDFFDERPE-----ISY 372
468 LETSIPYAPDMKICYCHGVGKPTERGYY-----TNNPEQGVIDSVDGTFKVENGIYW 522
373 GGDGDTVMNLVSL-LALQSLMKREKNQYLVKVIDGVSHST-----LKDEVALNEIYV----- 424
523 DGDGDTPLPLALGLVCNKKWQ-----TKRNPANTSTNYETIKHPAFLDGLGPR 573
425 --EITSINSHAEI 435
574 SAEHVDILGHSEL 586

RESULT 9

hypothetical protein F28D10_20 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51780
R:DeSensy, M.; Berger, C.; Cooke, R.; Grellet, F.; Landie, M.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, August 2000
A:Reference number: 225454
A:Accession: T51780
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-665
A:Cross-references: EMBL:AL391254
A:Experimental source: cultivar Columbia; BAC clone F28D10
C:Genetics:
A:Map position: 3
A:Introns: 132/2; 206/3; 302/2; 415/3; 504/2
A>Note: F28D10_20

Query Match

Best Local Similarity 7.0%; Score 163; DB 2; Length 665;
Pred. No. 6.9e-05;
Matches 117; Conservative 81; Mismatches 164; Indels 254; Gaps 28;

32 GASNDPLILIPG--NGGNQL-EARLTNQKPSFICESWYPLIKKNGMFLW--FDS 86
86 GVKAFHPVILVPGIYTGLEMEGRPCAE-----GIFRK-----RLMGASFSE 128
87 VILAFQCFARMTLHNGEIDDYFNTPGVETR-VPHGSGTNSLLIYLPRLKHTGYMA 145
129 ILRRPL-CWLEHLSIDSETGLD---PSGIRVRAVPGLVAAD-----YPA 168
146 P-----LVDSIQKIGYADGETLFGAPYDFRYGLAEGHPQOVGSKFLDKNLIEAS 198
169 PCYFAMAVLIEMLAKIGY-EGKNLMASIDWRLSF---HNFVARDQSLRLKSKTELWY 223
199 NSNNGKPVILLSHSLGGLFVLOLN--RNP-----PSWRKKEIKHFIALSAPWGS- 246
224 ATNGFKKVVVPHSMGAIYFHLFKMWETPLPDGGGGGPGCAKHKIKSVNIGPAFLV 283
247 --AIDEMT-----FASGTLGVPLVDPULV----- 271
284 PKAVSNLSAEGKDLAYARSLAPGLDSELLKQLEHLMRSHSWSIVSLPKGGEAI 343
272 -----DEORSE-----SNLMLLPKTFEGPK----- 294
344 WGDLSHAEEGLNCIYSKKSSQLSLNLIKONYSLKPSRKVEPKYGRIVSPGKRASE 403
295 -----PIVITPIRPYSAHMDVFL 313
404 LPSSQLSTLWKELSRVGNSNDSTSCGEFWEYEMSMRESYTKVAENATATATVYLDL 463
314 KDIG-----FPEGV-----YVETRLPLIGNIKAPQVPTICM 347
464 RPIARMKMRRAEAFHSHGIADLDLPKYGHYKYWNPLET-KLP-----EAPEMEMYCLY 517

348 GTGVGTFLETLFY-----GKGDPE-----RPEISYDGDGTYNLVSL-- 384
518 GVGIPIPERYIYIKLATSSCKKSSIPFRIDGSLDGDVCLKGSTRADDDESPVYSAGF 577
385 -----LALQSLMKREKNQ--YLVKVIDGVSHSTILKDEVALNEIYGEI 426
578 MCAKMGKGRKTRFNPSCMDQFLEBYKHKPPGSLLESNGTSGAHVDIM-GNVGLIEDVLI 636
427 TTSINSHAEIGLSNLF 442
637 AAGASQGEIGDRIYS 652

RESULT 10

hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86171
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86171
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <STO>
A:Cross-references: GB:AE005172; NID:q4204287; PIDN:AA010668.1; GSPDB:GNO0141
A:Genetics:
A:Map position: 1

Query Match

Best Local Similarity 6.3%; Score 147; DB 2; Length 552;
Pred. No. 0.001;
Matches 75; Conservative 48; Mismatches 124; Indels 64; Gaps 16;

8 GKIEVATLVTVVYVYVMSLCTGCA-----SNLDPLILIPNGNQL- 52
2 GANSKSVTASFYIVAVFLI---CGGRVAVDETEHGGYSKLSG-IIPGFASTYDLRW 57
53 -RLTNQKPSFICESWYPLIKKNGMFLWPDSSVILAPFTQCFARMTLHNGEIDDY 111
58 SLDCPYTPLDF-----NPLDVLWIDTQKLSA-VNCPKCV-----LDPY 98
112 FNTPGVETVPHFGSTNSLLIYLPRLKHTTGMAPIVDSLOK---LGYADGETLFGARY 167
99 NOTDHECKSRPDSGLSATTELDP--GYITGPLSTYWKEMLWCVEFG--TEANATVAVPY 155
168 DFRYGLAAGHPDSOVGSK--FLDKNLKLEASNSNGKPVILLSHSLG---LFW--- 218
156 DMRLS-----PTKEERDLVFRHKLKLTRETALKLKLG--PSIYFAISKGNVNFRTLEWL 208
219 -LQLNRNPSPWRKKEIKHFIALSAPWGAIDEMTYFASGNTLGVLPVLPVLRDQRSS 277
209 RLEIARKHVLMKLDQHIHAYFVAGVAPLDSVEAKIKSTLSGVTFGLP-VSEGTARLLSNSE 267
278 ESNLMLLPNK 288
268 ASSLWMLPFSK 278

RESULT 11

hypothetical protein T16H5.220 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 24-Nov-1999
C:Accession: T04767

R:Bevan, M.; De Haan, M.; Maarse, A.C.; Grievell, L.A.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, June 1998
A:Reference number: 215383

A:Accession: T04767

A:Molecule type: DNA

A:Residues: 1-493 <BEV>

A:Cross-references: EMBL:AL024486

A:Experimental source: cultivar Columbia; BAC clone T16H5

C:Genetics:

A:Map position: 4

A:introns: 82/1; 112/3; 152/2; 206/2; 283/3; 322/2; 340/3; 358/3

A:Note: T16H5.220

C:Superfamily: Arabidopsis thaliana hypothetical protein T16H5.220

Query Match 5.4%; Score 125.5; DB 2; Length 493;

Best Local Similarity 24.0%; Pred. No. 0.045;

Matches 50; Conservative 27; Mismatches 58; Indels 73; Gaps 10;

QY 35 NLDPILIPGNGQLEARLTNQKPSYPLIKKNG-----WFR----- 80

Db 30 NLNPVLIVPGIAGSILNA-----VDHENGNERVWVRLFGADHEFR 70

QY 81 --LW--PSS-----VILAPFQCPA--ERMILYHQELDDYFNTGCVETRPHEGSTSL 130

Db 71 TKMSRFRPSTGKTSIDPKTSIVVPDRAGLHAIDVD-----PDM-----IVGRBSV 119

QY 131 LYLPRLKHITGYMAPLVDSLOKLGADGETLFGAPYDFRYGLAEGHPSQVSKFLKDL 190

Db 120 YFPHMIVEMIGW-----GFEGKTLFGFGYDFRQSNRLQETLIDPAKR----- 163

QY 191 KNLIEASNSNNGKPVILLSHSLGLEV 218

Db 164 --LETVYKASGEKKINIVSHSMGGLV 188

RESULT 12
E86854
hypothetical protein oppa [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 24-Aug-2001

C:Accession: E86854

R:Boletín, A.; Wincker, P.; Manger, S.; Jallion, O.; Malame, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s.s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: E86854

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-600 <STO>

A:Cross-references: GB:AE005176; PID:912724867; PIDN:AAK05935.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: oppa

C:Superfamily: dipeptide transport protein

Query Match 4.8%; Score 113; DB 2; Length 600;

Best Local Similarity 21.9%; Pred. No. 0.6;

Matches 90; Conservative 58; Mismatches 159; Indels 104; Gaps 21;

QY 1 MKKQDEBLKLEVATLTATVYVVMLSLCTGASNLDPILIPGNGQLEARLTNQKP 60

Db 1 MKK-----LKV-----TLASSVYLAALLSACGS-----NONSTSTKRLKA 38

QY 61 STFICSWYPLIKKNGWFLMFD-----SVILAPFQCPAERMILYHQELDD-----Y 111

Db 39 GNFVAVNPNPKAIKGKGLTAIOSDSPKAEMLAPLS-----DDATGGS 83

QY 112 FNTGCVETRPHEGSTNSLILNPLRKHITGYMAPLVDSLOK-----LGYADG 159

Db 84 MSSPG-----GGQDLFTFTSSSKYING--GRANVSLYKDAKTATITLRKDLKMSDG 133

QY 160 ETLEGAPYDFRYGLAEGHPSQVSKFLKDLKNLIEASNSNNGKPV-----TLLSHSLG 215

Db 134 SEVTAKEYEFSYDLTA--NPAYGSDRWTDLSANIV-GLSDYHAGKAKTISITPPDGENG 190

QY 216 LEVLQILNRNPSPMRKFKIFKFIALSAWGAID--EMYTPASGWTGLVPLVDLIVDE 273

Db 191 KVIAKQFKEMTPGMNQTNGTFLEIVAPYOLKDYAPKDIASRSKSTTKPLVTPGPKFN 250

QY 274 QRSESNLMLPNPKIFGQPKR-----IVIT--PIRPSADMDVFLDKFGPEGVY 323

Db 251 VVAGES--IKYVNPYYWG--EKPKLNSITYEIVSTAKSVAALSAH-KYDYINDMRASO--- 304

QY 324 PYETRIPLIGNIKARQVPTICIMGTGVTLETIFYGSGDDEPEREISYCD 374

Db 305 -YKQ-----VKDYKGYK-----LQQLYISLMTYLGHYDKKSISSVOD 344

RESULT 13

T44608
pyruvate carboxylase (EC 6.4.1.1) [imported] - Bacillus cereus (fragment)

C:Species: Bacillus cereus

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Sep-2000

C:Accession: T44608

R:Okstad, O.A.; Hegna, I.; Lindbaek, T.; Rishovd, A.L.; Kolsto, A.B.

Microbiology 145, 621-631, 1999

A:Title: Genome organisation is not conserved between Bacillus cereus and Bacillus su

A:Reference number: 422811; MUID:99231848; PMID:10217496

A:Accession: T44608

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-984 <OKS>

A:Cross-references: EMBL:AJ010111; NID:94584147; PIDN:CAB40604.1; PID:94584148

A:Experimental source: ATCC 10987

C:Genetics:

A:Note: PYCA

C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-biotin

C:keywords: ligase

Query Match 4.7%; Score 109; DB 2; Length 984;

Best Local Similarity 17.9%; Pred. No. 2.6;

Matches 104; Conservative 94; Mismatches 204; Indels 178; Gaps 24;

QY 13 VATLVTVVYVVMLSLCTGASNLDPILIPGN-----GNGQLARLTNQKPSYPLIKKNG 67

Db 140 ITEMITGVIVQSLTLADGHALSKLVGPKQEBVVVHGFIQSRVTTEDPLNNFMPT 199

QY 68 WYPLIKKNGWFLMFD-----SVILAPFQCPAERMILYHQELDDY-----FN 113

Db 200 GKMAVYRSGGFGVRLDIGNSGFQAGVITPYDLSLVKVTVALFPEQAAKMERLKEFR 259

QY 114 TPQVETRPHEGSTNSLILNPLRKH--ITG-YMAPLVDS-----LQKLG 155

Db 260 IRGIKTNIP-----FLENVYKHKNFLSGEYDTSFIDASPFLFLFSKRKRDGTYMLN 310

QY 156 YADETLFGAP-----YDFRYGLAEGHPSQVSKFLK----- 189

Db 311 YIGTVVNGFPVGCKEKPDPDAKIPNVLSHSEPILOKIDBERGADGLVKWVQDKR 370

QY 190 -----LKNLIEASNSNNGKPVILLSHSLG----- 215

Db 371 VLNDTFRDAGHSLATRIKTLHQIAEPTARMLPRLFAEMMGATPDVAYRFLKED 430

QY 216 -----LFLVQLILNRNPSPMRK--KFKIFKFIALSAWGAIDEMYTTPASG 257

Db 431 PWERILLDREKMPNVLFQMLRSSNAVGYKNYPNLIQKFEVCEAQAQ--IDVERIPDSL 488

QY 258 NTLGVPPLVDPLLVDEQRSSSNLML--LNP-----KTFGR 292

Db 489 NWVEGMRAIDAVIDGTGIAETACYTGDIHDPRLSKYDLNLYNNLAKELASGARILGI 548

QY 293 QKPIVITPIRPSADMDVFLK--IGFPEGVYETR--ILPLIGNIKA--POVPI 344

Db 549 KDMAGL--LKNMAVYDLVSAKETEVSIPILHATHDTSNGILTYTKAIEAGVDIVDAVS 606

QY 345 CIMG-TGVGTLETIFYGSGDDEPEREISYGDGDTNVLVSLALQSLMKKEKNQYLKVV 403

Db 607 SWAGTSPSANTLYALCGNERQPD-----VNIDSLERLSHYMEDVRKYAPFES 657
 QY 404 IDGVSHSTLKDEVALNEIV-GEITSINSHAE-LGSLNFP 441
 Db 658 GNNAPRT-----EYVNHMPGGQYSNMQQAKAVGLGDRF 692

RESULT 14

B70013
 hypothetical protein yuII - Bacillus subtilis

C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
 C:Accession: B70013

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E.
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gall
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y.M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle
 Rieger, M.; Rivolta, C.; Rocha, A.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A.; Authors: Schleich, S.; Schroeter, R.; Scifone, F.; Sekiguchi, J.; Sekowska, A.; Serot
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunori, K.; Yata, K.; Yoshida, K
 A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:9804033; PMID:9384377

A:Accession: B70013

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-314 <KUN>

A:Cross-references: GB:299120; GB:AL009126; MID:92635613; PIDN:CAB15191.1; PID:el184280;

A:Experimental source: strain 168

C:Genetics:

A:Gene: yuII

Query Match 4.6%; Score 106.5; DB 2; Length 314;
 Best Local Similarity 21.9%; Pred. No. 0.78;
 Matches 65; Conservative 34; Mismatches 109; Indels 89; Gaps 12;

QY 71 LKKKNGWRLMFDSSVILAPFOCAEMTLHYQELDDYNTPEVERVPH----- 123
 Db 4 LVDSENHITLRF--LKRMSYCKMEQTTDRTNGTSTNAFTIPETEVMMSSRNEKPT 60
 QY 124 -----FGTNSLLYLNPRLKHTGYAPVDSLOKIG 155
 Db 61 YHIFSKPSTPPAGYPIYILLDANSVGTMEANRIGRRPEKTVPAVIG---IG 117
 QY 156 YADGETLFGAPY-DFRYGLAEGHPSOVGS-----KFL-KDLKMLIEASNS 200
 Db 118 YETAEFFSARRHDEFTMPAOSKILPERDREMPHEGAEFGFTEEDLKPEIERDYQI 177
 QY 201 NNGKXVILLSHSLGLFVQLNRP-----PS--WKKKF-----KPIALSAPW 244
 Db 178 DKKRQTI-FGHSGLGFLVQLVLTTRPDARQYIAGSPSIHMNKPFLIKTKTDHFSVLTJKN 236
 QY 245 GGAID-----EMTFASGNTLGLVPLVPLVREOR-----SSESNTMLLP 285
 Db 237 NQPIVILLAGLEQHHKSRMDNARELYERLAVLSQGIKRAEFCFSGEGHISVLP 293

RESULT 15

S73355

excinuclease ABC chain C - Mycoplasma pneumoniae (strain ATCC 29342)

N:Alternate names: hypothetical protein C09_orf586; virc protein

C:Species: Mycoplasma pneumoniae

A:Variety: ATCC 29342

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Dec-1999

C:Accession: S73355

R:Himmelfreid, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996

A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon

A:Reference number: S73327; MUID:97105885; PMID:8948633

A:Accession: S73355

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-586 <HIM>

A:Cross-references: EMBL:AE000004; GB:U00089; MID:91673671; PIDN:AAB95677.1; PID:9167

A>Note: The nucleotide sequence was submitted to the EMBL Data Library November 1996

C:Genetics:

A:Gene: uvrC

A:Genetic code: SGC3

A:Start codon: TTG

C:Superfamily: excinuclease ABC chain C

C:Keywords: DNA repair; hydrolase

Query Match 4.5%; Score 106; DB 1; Length 586;
 Best Local Similarity 22.2%; Pred. No. 2.1;
 Matches 106; Conservative 58; Mismatches 161; Indels 152; Gaps 24;

QY 34 SNIDPLILPGNGNOLARLNOYRPTFCESWYPLIKKNGWRLMFDSSVILAPPT 93
 Db 64 ADVEYILKKNENDALNEMALKIKYKPRNL-----VLKENGYLYFFITASY----- 111
 QY 94 QCAEEMTL-----HYQELDDYNTPEVERVPHGSTNSLYLNPRLK---HTGYMAP 146
 Db 112 -----KPTLELGRYEFKSKKNTFG-PFASKFRLRDIYDLKLFLPKCAPRERGHGPF 165
 QY 147 LVDLSLOKLGADSE-----TLFGAPYDFRGLAEGHPSOVGSKFLDKLNLIEAS 198
 Db 166 YVLLKMGKMGCGMEDTPERTQTVKIGIEQFNHG-----PEQY-----LNHLQOQETKAS 215
 QY 199 NSNNGRPVLLSHSLG-GLFVLOLLNRPNSWKKRFKH-FIALSAPMGGAIDEMTFAS 256
 Db 216 EQGNFEAA---RHFLDLQKAVLELVNMQGTAFIKAKOSHDFIG-----YVFEX 260
 QY 257 GNTLGVPL---VDPLVY-----RDEQR-----S 277
 Db 261 -NVLAITVAAYVDNOLIGKNOQVLELPODEKVESALVTFIHYYSKTKIPKTLTVSL 319
 QY 278 ESNLWLLPN-----PKIFGPQKPIVITPIRYSAHMDVDFLKDIGPEGVYPTETRI 329
 Db 320 EENLSILANSIKINYQPK-NGEQKSILOTV-----DNARYALNTKW 361
 QY 330 LPLIGNIKAPQVPTICMGVGTLETLFYGKGFDERPEISYGDGTYNIVLSLALOS 389
 Db 362 TGFNNLNRAEYHQALQLQVPSIQSL-----EIDISFYDKDHVG-----A 405
 QY 390 LKKEENQYLUK-----VKIDGSHSTSLKDEVALNEIVGELTTSINSHAEGLSNL 440
 Db 406 MLREYENGKRWKALSRRYININIDHKGDTNYMAD--VVYRRI---ISSIOTKHQPLPSDL 458

Search completed: February 11, 2003, 19:15:48
 Job time : 25 secs

RA Hisson J.E., Driscoll D.M., Birnbaum S., Britten M.L.:
RT "Baboon lecithin cholesterol acyltransferase (LCAT): cDNA sequences
of two alleles, evolution, and gene expression.";
RL Gene 128:295-299(1993).
CC -1- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
CC LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
CC CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + a sterol - a sterol
CC ester + 1-acylglycerophosphocholine.
CC -1- ENZYME REGULATION: Apolipoprotein A-I IS A POTENT ACTIVATOR FOR
CC THIS ENZYME.
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LIVER AND CEREBELLUM.
CC -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
CC LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC -----
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CC -----
DR EMBL; L08633; AAA35388.1; -;
DR PIR; JCI502; JCI502.
DR InterPro; IPR003386; LACT.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF02450; LACT; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KM Transferrase; Acyltransferase; Lipid metabolism; Glycoprotein; Signal.
FT CHAIN 1 24
FT SIGNAL 25 440
FT FT
FT ACCT SITE 205 205
FT DISULFID 74 98
FT DISULFID 337 380
FT CARBOHYD 44 44
FT CARBOHYD 108 108
FT CARBOHYD 296 296
FT CARBOHYD 408 408
SQ SEQUENCE 440 AA; 49645 MW; E06B0C8300BA59D CRC64;

Query Match 23.0%; Score 537; DB 1; Length 440;
Best Local Similarity 33.3%; Pred. No. 2.5e-35;
Matches 129; Conservative 73; Mismatches 163; Indels 22; Gaps 11;

OY 38 PLILPGNGNOLLEARNLNOYKPSFFICESSWYPLIKKNGWRLMFDSSVILAPPTQCPA 97
Db 48 PYILVPGCLGNLEAKLD---KPDVY---NMW-CYRKTEDFTTILDLNMFPLGVDGMT 100
OY 98 ERMFLHYHQELDDYFNTPGEVETRVPHFGSTNSLYLNPRLKHITGYMAPLVDSLOKGYA 157
Db 101 DNTRVVYNRSSGLVSNAGVQIRVGFCKTYSVEYLD--SKLAVLYHTLVQNLNMGV 158
OY 158 DGETLFGAPYDFRGLAEGHPQYQSGKFLDKLKLDEASNSNNGKYYILLISHLGLF 217
Db 159 RDEYVRAAPYWRLL-----EPGQ-QEERYKHLGLVEE-MMAAGKKEVFLGSHGLGILH 210
OY 218 VLOLLNRPSPMRKKEIKHFIATLSAPMGAGIDEMTFASNGTILGVLDPDLVREORSS 277
Db 211 LLYFLRROPQAMKDRFIDGFTSLGAPMGSGTKPMLVLSGDOGIPIMSSIKLKEQRIT 270
OY 278 ESNMLLPNPIFGPKQKIVITPRVSAHMDVFLDKDIGEPGEGYPP-ETRIILPLINNI 336
Db 271 TTPMMPFSRLAMPEDHVFISPSFNVTGRDQRFQFALHFEEGYVMLOSR--DLLAGL 328
OY 337 KAPOVPTICMGTVGVTLETFYKGG-DPDERPEISYDGDGTVLVSLALQSIIMKEEK 395
Db 329 PAPGEVYCLYGVGLPRTYIYDHGEPYTDVPLVLEDCDVTATRS--TELCGLMGQRQ 387
OY 396 NOYLKVVKIDGVSHRSILKDEVALNEI 422
Db 388 POPVHLPLRGIOHLNMFVSNQTELEH 414

RESULT 4
LCAT_MOUSE
ID LCAT_MOUSE STANDARD: PRT: 438 AA.
AC P16301;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphatidylcholine-sterol acyltransferase precursor (EC 2.3.1.43)
DE (Lecithin:cholesterol acyltransferase) (Phospholipid:cholesterol
DE acyltransferase).
DE LCAT.
GN LCAT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90094326; PubMed=2600083;
RA Warden C.H., Langner C.A., Gordon J.I., Taylor B.A., McLean J.W.,
RA Lusis A.J.;
RT "Tissue-specific expression, developmental regulation, and
RT chromosomal mapping of the lecithin: cholesterol acyltransferase
RT gene. Evidence for expression in brain and testes as well as liver.";
RL J. Biol. Chem. 264:21573-21581(1989).
RN [2]
RP SEQUENCE OF 1-14 FROM N.A.
RA Merion G., Margaretti N., Magnaghi P., Taramelli R.;
RL Submitted (May-1992) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
CC LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
CC CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + a sterol - a sterol
CC ester + 1-acylglycerophosphocholine.
CC -1- ENZYME REGULATION: Apolipoprotein A-I IS A POTENT ACTIVATOR FOR
CC THIS ENZYME.
CC -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
CC LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC -----
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DR EMBL; J05154; AAA39419.1; -;
DR EMBL; X54095; CAA38029.1; -;
DR PIR; A34158; XMSN.
DR MGD; MGI:96755; Lcat.
DR InterPro; IPR003386; LACT.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02450; LACT; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KM Transferrase; Acyltransferase; Lipid metabolism; Glycoprotein; Signal.
FT CHAIN 1 24
FT SIGNAL 25 438
FT FT
FT ACCT SITE 205 205
FT DISULFID 74 98
FT DISULFID 337 380
FT CARBOHYD 44 44
FT CARBOHYD 108 108
FT CARBOHYD 296 296
FT CARBOHYD 397 397
FT CARBOHYD 408 408
SQ SEQUENCE 438 AA; 49765 MW; 2FD57194343136 CRC64;

Query Match 22.1%; Score 516; DB 1; Length 438;
Best Local Similarity 33.0%; Pred. No. 1.2e-35;

RL Nucleic Acids Res. 18:5308-5308(1990).
 CC -1- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
 CC LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
 CC CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + a sterol = a sterol
 CC ester + 1-acylglycerophosphocholine.
 CC -1- ENZYME REGULATION: Apolipoprotein A-1 IS A POTENT ACTIVATOR FOR
 CC THIS ENZYME.
 CC -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
 CC LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, X54096; CAA38030.1; -.
 CC PIR, S11214; XXRTN.
 CC InterPro: IPR003386; LACT.
 CC InterPro: IPR000734; Lipase.
 CC InterPro: IPR000379; Ser_estcrs.site.
 CC Pfam: PF02450; LACT; 1.
 CC PROSITE: PS00120; LIPASE_SER; 1.
 CC TRANSFERRASE: Acyltransferase; Lipid metabolism; Glycoprotein; Signal.
 CC SIGNAL 1 24
 CC FT CHAIN 25 440 PHOSPHATIDYLCHOLINE-STEROL
 CC FT ACTL_SITE 205 205 ACYLTRANSFERASE.
 CC FT DISULFID 74 98 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT CARBOHYD 337 380 BY SIMILARITY.
 CC FT CARBOHYD 44 44 N-LINKED (GLCNAG. . .) (POTENTIAL).
 CC FT CARBOHYD 108 108 N-LINKED (GLCNAG. . .) (POTENTIAL).
 CC FT CARBOHYD 296 296 N-LINKED (GLCNAG. . .) (POTENTIAL).
 CC FT CARBOHYD 397 397 N-LINKED (GLCNAG. . .) (POTENTIAL).
 CC FT CARBOHYD 408 408 N-LINKED (GLCNAG. . .) (POTENTIAL).
 CC SEQUENCE 440 AA: 49727 MW: 655392121684885 CRC64;
 Query Match 22.0%; Score 514; DB 1; Length 440;
 Best Local Similarity 32.8%; Pred. No. 1,7e-33;
 Matches 128; Conservative 75; Mismatches 159; Indels 28; Gaps 12;

RESULT 7
 LOCAT_TATKG STANDARD: PRT; 293 AA.
 AC 035840:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphatidylcholine-sterol acyltransferase (EC 2.3.1.43) (Lecithin-
 DE cholesterol acyltransferase) (Phospholipid-cholesterol
 DE acyltransferase) (Fragment).
 GN LCAT.
 OS Tatera kempii gambiana (Kemp's gerbil).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 OC Tatera.
 OX NCBI_TaxID=41264;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98086782; PubMed=9417899;
 RA Robinson M., Catzeffis F., Briolay J., Mouchiroud D.;
 RT "Molecular phylogeny of rodents, with special emphasis on murids:
 RT evidence from nuclear gene LCAT".
 RL Mol. Phylogenet. Evol. 8:423-434(1997).
 CC -1- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
 CC LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
 CC CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + a sterol = a sterol
 CC ester + 1-acylglycerophosphocholine.
 CC -1- ENZYME REGULATION: Apolipoprotein A-1 IS A POTENT ACTIVATOR FOR
 CC THIS ENZYME (BY SIMILARITY).
 CC -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
 CC LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, U72298; AAB58989.1; -.
 CC DR EMBL, U72297; AAB58989.1; JOINED.
 CC DR InterPro: IPR003386; LACT.
 CC DR InterPro: IPR000734; Lipase.
 CC DR Pfam: PF02450; LACT; 1.
 CC PROSITE: PS00120; LIPASE_SER; 1.
 CC TRANSFERRASE: Acyltransferase; Lipid metabolism; Glycoprotein.
 CC NON_TER 1 1
 CC FT ACTL_SITE 123 123 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT CARBOHYD 26 26 N-LINKED (GLCNAG. . .) (POTENTIAL).
 CC FT CARBOHYD 179 179 N-LINKED (GLCNAG. . .) (POTENTIAL).
 CC FT CARBOHYD 280 280 N-LINKED (GLCNAG. . .) (POTENTIAL).
 CC FT NON_TER 293 293
 CC SEQUENCE 293 AA: 33822 MW: 86FB4BB7CA1738B7 CRC64;
 Query Match 15.2%; Score 354; DB 1; Length 293;
 Best Local Similarity 29.2%; Pred. No. 5.6e-21;
 Matches 98; Conservative 57; Mismatches 129; Indels 52; Gaps 10;

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Db 137 GIPIMSSIKREBORITTTSPMMFPDRDVPEDHVFISPEFNVTGODEFERFSIDLHFE 196
Qy 321 GYPPY-ETRIPLPLIGNIKAPQVITTCMGVGTLETLFYKGDPDEREIS--YDDSGG 377
Db 197 GYMWYMFQSR--DLLEGLPAPGVVCLYGVGRPTRYTYIDHNFPYKDPVALYEDGD 253
Qy 378 TVNLVSLALQSLMKKEKNQYLKVKVKGDSHTSL 413
Db 254 TVATRS--TELCGOMOGROSQPVYLLPMNGDHLNMV 288

RESULT 8
LCAT_MICMN STANDARD: PRT: 299 AA.
AC 035724:
Dt 30-MAY-2000 (Rel. 39, Created)
Dt 30-MAY-2000 (Rel. 39, Last sequence update)
Dt 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphatidylcholine-sterol acyltransferase (EC 2.3.1.43) (Lecithin-
DE cholesterol acyltransferase) (Phospholipid-cholesterol
DE acyltransferase) (Fragment).
GN LCAT.
OS Micromys minutus (European harvest mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Micromys.
OX NCBI_Taxid=13151;
RN SEQUENCE FROM N.A.
RA MEDLINE-98086782; PubMed-9417899;
RX Robinson M., Catzeffis F., Briolay J., Mouchiroud D.;
RT "Molecular phylogeny of rodents, with special emphasis on murids:
RL Mol. Phylogenet. Evol. 8:423-434(1997).
CC -1- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
CC LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
CC CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + a sterol = a sterol
CC ester + 1-acylglycerophosphocholine.
CC -1- ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
CC THIS ENZYME (BY SIMILARITY).
CC -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
CC LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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CC -----
DR EMBL: U72294; AAB58988.1; -.
DR EMBL: U72293; AAB58988.1; JOINED.
DR InterPro: IPR003386; LACT.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF02450; LACT; 1.
DR PROSITE: PS00120; LIPASE_SER; FALSE_NEG.
KW Transferase; Acyltransferase; Lipid metabolism; Glycoprotein.
FT NON_TER 1
FT CAROHD 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHD 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHD 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHD 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 299
SQ SEQUENCE 299 AA: 34833 MW: 55896C9A38C2482C CRC64:

Query Match 14.7%; Score 342.5; DB 1; Length 299;
Best Local Similarity 27.8%; Pred. No. 4.7e-20;
Matches 94; Conservative 61; Mismatches 136; Indels 47; Gaps 10;
Qy 78 NPLMFSSVILAPFTQCFAERWTLHYHQELDDYFNTPGVETRVPHFGSTNSLLYNPL 137

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Db 1 FETIMIDINMFLPLGVDCWIDNTRVYNNRSGRMSNAPGVQIIRVPFGKTYSEYLD-- 58
Qy 138 KHTGTMAPLVDSLOKLGADGETLFGARYDPRTYGLAAGHPQVSKELKDLKNIIEA 197
Db 59 NKIAGYLHLYVOLLVNNAAVYRDVTRAPADWRLA-----PSQ--ODEYYOKIAELVEEM 111
Qy 198 SNSNKKRPYLLSHSGGLEFVLQDLNRNPPSWMKRFIKHFIALSADWGAIDEMYFASG 257
Db 112 YDA-YKRPVFLIHRIGCLHVLHFLHQ--SMK----- 141
Qy 258 NPLGVPLVDPLVRDORSESNNMLLPNPKIFGPQPIVTPIRPYSAHDWVFLKDIG 317
Db 142 --GIPIMSNIKREBORITTTSPMMFPDRDVPEDHVFISPEFNVTGODEFRFPADLH 198
Qy 318 FPEGYPPY-ETRIPLPLIGNIKAPQVITTCMGVGTLETLFYKGK-DEDEREISYGG 375
Db 199 FEGGWYMFQSR--DLLEGLPAPGVVCLYGVGRPTRYTYIDHNFPYKDPVALYEDG 256
Qy 376 DGVNLVSLALQSLMKKEKNQYLKVKVKGDSHTSL 413
Db 257 DETVATRS--TELCGOMOGROSQPVYLLPMNGDHLNMV 293

RESULT 9
LCAT_ELIOU STANDARD: PRT: 299 AA.
AC 03573:
Dt 30-MAY-2000 (Rel. 39, Created)
Dt 30-MAY-2000 (Rel. 39, Last sequence update)
Dt 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphatidylcholine-sterol acyltransferase (EC 2.3.1.43) (Lecithin-
DE cholesterol acyltransferase) (Phospholipid-cholesterol
DE acyltransferase) (Fragment).
GN LCAT.
OS Elomys macrurus (Garden dormouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Myoxidae; Leithinae;
OC Elomys.
OX NCBI_Taxid=53277;
RN SEQUENCE FROM N.A.
RA MEDLINE-98086782; PubMed-9417899;
RX Robinson M., Catzeffis F., Briolay J., Mouchiroud D.;
RT "Molecular phylogeny of rodents, with special emphasis on murids:
RL Mol. Phylogenet. Evol. 8:423-434(1997).
CC -1- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
CC LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
CC CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + a sterol = a sterol
CC ester + 1-acylglycerophosphocholine.
CC -1- ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
CC THIS ENZYME (BY SIMILARITY).
CC -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
CC LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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CC or send an email to license@sdb-sib.ch).
CC -----
DR EMBL: U72316; AAB58999.1; -.
DR EMBL: U72315; AAB58999.1; JOINED.
DR InterPro: IPR003386; LACT.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF02450; LACT; 1.
DR PROSITE: PS00120; LIPASE_SER; FALSE_NEG.
KW Transferase; Acyltransferase; Lipid metabolism; Glycoprotein.
FT NON_TER 1

```

FT ACT_SITE 127 127 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 299 299
 SO SEQUENCE 299 AA; 34653 MW; 9C2041FE79A2CEFC CRC64;
 Query Match 14.6%; Score 341; DB 1; Length 299;
 Best Local Similarity 27.6%; Pred. No. 6,2e-20;
 Matches 93; Conservative 59; Mismatches 137; Indels 48; Gaps 9;
 QY 79 FRLMFDSSVILAPFTQCFAERMTLHYHQELDDYFNTGCVETRPVPHGSGTSLSLYLNPRLK 138
 DB 4 FTIMDLNMFSLGVDYCDIDNTRVYNNRSGSYMANPQVQIRVPGFKTYSVEYLD--N 61
 QY 139 HITGMAPLVDSLOKLGADGETLFGAPYDFRYGLAEGHPQVSGSKFLDKNLIEEAS 198
 DB 62 KLAGMHTLVQNLVNNKAVRDETVAPRYDMRL-----EPHQOEYLYLK-LAGLYEE-M 113
 QY 199 NSNNGRPVILLSHSLGGLFVYLQLLNRPNSMRKKFIKHFIALSAPWGGAIDEMYTPASGN 258
 DB 114 YATYGRPVFLIGHSLGFCHELLYFLLOPQ----- 142
 QY 259 TLGVPVLVPLVRDQSSSESNMLLPNPKITFGPKPIVITPIRYSAHMDVFLKDIOG 318
 DB 143 --GLPIMSSIKLVERQRTTTSPPMFPSPHQVPEDEHVFISTPNNFYTESDFQRFPLDAF 200
 QY 319 PEGVYPR-ETRIPLPLGNIRAKPOVPTICMGTVGTLETLFYGKG-DDEPEREISGDGD 376
 DB 201 EDGWMMLQSR--DLLAGLPAPGVEVYCLYGVLPTPTTYMDHGFPTTDPVGIITYEDGD 258
 QY 377 GTVNLVSLAIQSLKKEKNQYLVKIDGVSHSIL 413
 DB 259 DTVTTHS-TELCSHWGROQPQPVHLLPLRGTOHLNMY 294
 RESULT 10
 LCAT_CLEGL STANDARD: PRT; 291 AA.
 ID LCAT_CLEGL
 AC 035502;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphatidylcholine-sterol acyltransferase (EC 2.3.1.43) (Lecithin-
 cholesterol acyltransferase) (Phospholipid-cholesterol
 acyltransferase) (Fragment).
 DE LCAT.
 GN Clathromyxa glareolus (Bank vole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
 OC Clethrionomys.
 OX NCBI_TaxID=51090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98086782; PubMed=9417899;
 RA Robinson M., Catefellis F., Briolay J., Mouchiroud D.;
 RT "Molecular phylogeny of rodents, with special emphasis on murids:
 RT evidence from nuclear gene LCAT".
 RL Mol. Phylogenet. Evol. 8:423-434(1997).
 CC -1- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
 CC LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
 CC CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + a sterol -> a sterol
 CC ester + 1-acylglycerophosphocholine.
 CC -1- ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
 CC THIS ENZYME (BY SIMILARITY).
 CC -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
 CC LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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 DR EMBL; U72300; AAB58990.1; -. JOINED.
 DR EMBL; U72299; AAB58990.1; JOINED.
 DR InterPro; IPR003386; LACT.
 DR InterPro; IPR000734; Lipase.
 DR Pfam; PF02450; LACT; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Transferase; Acyltransferase; Lipid metabolism; Glycoprotein.
 FT NON_TER 1 1
 FT ACT_SITE 125 125 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 291 291
 SO SEQUENCE 291 AA; 33536 MW; B1F7E9DB8201219D CRC64;
 Query Match 13.9%; Score 323.5; DB 1; Length 291;
 Best Local Similarity 28.5%; Pred. No. 1.5e-18;
 Matches 87; Conservative 53; Mismatches 112; Indels 53; Gaps 9;
 QY 78 WFLMFDSSVILAPFTQCFAERMTLHYHQELDDYFNTGCVETRPVPHGSGTSLSLYLNPRLK 137
 DB 1 FFTFLDNLMLFALGVCNMDNTRVYNNRSGRMSNAPCVQIRVPGFKTYSVEYLD-- 58
 QY 138 KHITGYMAPLVDSLOKLGADGETLFGAPYDFRYGLAEGHPQVSGSKFLDKNLIEEA 197
 DB 59 NKLACGMHTLVQNLVNNKAVRDETVAPRYDMRL-----EPHQOEYLYLK-LAGLYEE-M 110
 QY 198 NSNNGRPVILLSHSLGGLFVYLQLLNRPNSMRKKFIKHFIALSAPWGGAIDEMYTPASG 257
 DB 111 MHAAGKFPVFLIGHSLGFCHELLYFLLOPQ----- 134
 QY 258 NTLGVPVLVPLVRDQSSSESNMLLPNPKITFGPKPIVITPIRYSAHMDVFLKDIOG 317
 DB 135 -NGPLPIMSSIKLREQRTTTSPPMFPSPHQVPEDEHVFISTPNNFYTESDFQRFPLDAF 193
 QY 318 PEGVYPR-ETRIPLPLGNIRAKPOVPTICMGTVGTLETLFYGKG-DDEPEREISGDGD 374
 DB 194 FEEGWMMLQSR--DLLAGLPAPGVEVYCLYGVLPTPTTYMDHGFPTTDPVGIITYEDGD 250
 QY 375 GDGVY 379
 DB 251 GDDPV 255
 RESULT 11
 PDAT_SCHPO STANDARD: PRT; 623 AA.
 ID PDAT_SCHPO
 AC 094680;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Potential phospholipid:diacylglycerol acyltransferase (EC 2.3.1.158)
 DE (PDAT).
 GN Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Rattwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Obell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbinoiwtsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymompiez B.,
 RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Nuer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Coffeau A., Cadieu E., Diano S., Gloux S., Lelaure V., Mottier S.,
 RA Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovskiy G.V., Usseery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: Triacylglycerol formation by an acyl-CoA independent
 pathway. The enzyme specifically transfers acyl groups from the
 CC sn-2 position of a phospholipid to diacylglycerol, thus forming
 CC an sn-1-lysophospholipid (by similarity).
 CC -1- CATALYTIC ACTIVITY: Phospholipid + 1,2-diacylglycerol =
 CC lysophospholipid + triacylglycerol.
 CC -1- SIMILARITY: SOME, TO MAMMALIAN PHOSPHATIDYLCHOLINE-STEROL O-
 CC ACYLTRANSFERASE.
 CC -----
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 CC -----
 DR EMBL: AL035263; CAA22887.1; -
 DR InterPro: IPR003386; LACT.
 DR Pfam: PF02450; LACT; 1.
 KW Hypothetical protein; Transferase; Acyltransferase; Transmembrane.
 FT DOMAIN
 FT 11 14 POLY-LYS.
 FT TRANSMEM 57 77 POTENTIAL.
 SQ SEQUENCE 623 AA; 69748 MW; 1140ED8D46968C90 CRC64;
 Query Match 7.8%; Score 181; DB 1; Length 623;
 Best Local Similarity 22.1%; Pred. No. 9,7e-07;
 Matches 109; Conservative 65; Mismatches 171; Indels 148; Gaps 24;
 QY 38 PLILIPNGNGNOLLEARLTNOYKPSFTICESW-----YPLIKRKNQWFRILMPDSSVILAP 91
 Db 147 PVLIVPGVIVSSGL-----ESMSFNKCSIPYFRK-----RLMGSMMLKAM 166
 QY 92 F--TQCFAEKMTLHYHOELDDYNTPEQVETRVPH-FGSTNSLLYLNRKLHITGY--MAP 146
 Db 187 FLDKQCMLEHLMMDKRTGLD---PGGIKRLAAQGEAALFF-----ITGYTWMSK 233
 QY 147 LVDSLOKLGVADETELGAFYDFRYGLAAGHPSOYGSKRLDKLNLEASNSNNKXP 206
 Db 234 VINLALAIIG-EPNNMISASTYDKRLSYA---NLEBPKTFPSKLMFT-EYSNIVHKKV 287
 QY 207 ILSHSLGGLFVLQL-----NRNPSMRKKFKIHFALPSALPAGWGAIDEMYTEASG- 257
 Db 288 VLSHSGSGSVYTYFFPKWVAEGYNGGPTWVDHIEAFINIGSLGLGAKRTVAALLSGE 347
 QY 258 -NVLGVPVLDPLLVLRDQSSSESNL-----WLPNPKRIFGQ----- 293
 Db 348 MKDTGVITLNLIEKFFSRERAMVMTGWSMMLPKGADVAPDDLQNTFSGAIIRY 407
 QY 294 KPIVIRPIREYSADHWDFEIKDI-----GPPEGVYPTETRL-----P 331
 Db 408 REIDIDKHDEFDIDALQFLKNTYDDDFKMYLAKNYSHGILAMTEKEVELKNNEMPSKINP 467
 QY 332 LIGNIK-APQVPITCIMGTVGTLLETLFYGKGFDERPE-----ISY 372

Db 468 LERSLPAPDMKITYCHGVGKPTERGYY-----TNNPEGQPIDSSVNDGTRKENGIIYW 522
 QY 373 GDDGQVNVLSL-LALQSLMKEEKNOYLKVKIKDGYSHSI-----LKDEVALNEIYG---- 424
 Db 523 DDDGTLPLIALGLVCKRWQ-----TKRFPNPANSTIYKIEHPAADLGGPR 573
 QY 425 --EITSINSHAEI 435
 Db 574 SAEHVILHSEL 586
 RESULT 12
 ID UVRC_MYCPN STANDARD; PRT; 586 AA.
 AC P75350;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Excluclease ABC subunit C.
 GN UVRC OR MPN125 OR MP029.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RP [1]
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Haimelreich R., Halbert H., Plagens H., Pirkl E., Li B.-C.,
 RT Hermann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RL Nucleic Acids Res. 24:4420-4449(1996)
 CC -1- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
 CC CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
 CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). ATTACHES TO THE
 CC UVRA-UVRB COMPLEX, DISPLACING UVRA, AND THE DAMAGED DNA STRAND IS
 CC NICKED ON BOTH SIDES OF THE DAMAGED SITE (BY SIMILARITY).
 CC -1- SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRC.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE UVRC FAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AE000004; BAB95677.1; -
 DR InterPro: IPR004791; UVRC.
 DR InterPro: IPR001162; UVRC_C.
 DR InterPro: IPR000305; UVRC_N.
 DR Pfam: PF01541; Excl_endo_N; 1.
 DR ProDom: PD005870; UVRC_C; 1.
 DR SMART: SM00465; GYIC; 1.
 DR TIGRMAP: TIGR00194; uvrc; 1.
 KW SOS response; Excision nuclease; DNA repair; Complete proteome.
 SQ SEQUENCE 586 AA; 67771 MW; 6A495512C3447C81 CRC64;
 Query Match 4.5%; Score 106; DB 1; Length 586;
 Best Local Similarity 22.2%; Pred. No. 0.86;
 Matches 106; Conservative 58; Mismatches 161; Indels 152; Gaps 24;
 QY 34 SNDDPLILIPNGNGNOLLEARLTNOYKPSFTICESWYPLIKRKNQWFRILMPDSSVILAPFT 93
 Db 64 ADVEYVLTKNDALNLEAKLIKQYKRFNL-----VLKENNGYLYFFITASY----- 111
 QY 94 QCAERKTL-----HYHOELDDYNTPEQVETRVPHFGSTNSLLYLNRKL---HITGYMAP 146
 Db 112 -----KPTLGLGRYERSKKNRYFG-PPASSKFRILRDYLLKLFLPKCAHPERHGPCP 165

147 LVDSLOKLGADGE-----TLGAPYDFRYGLAEGHPGSOVSKFLDKNLIIEAS 198
166 YVOLKMKMGCEGDEPERYQTTVKIGIEQFNNH-----PEQV-----LNHLQOQCEIKAS 215
199 NSNNGKPVLLSHSLG-GLFVQLNLNRNPPSRKKFIKH-FIALSAPMGALDEMTFAS 256
216 EDOGNFPA--RHFIDLQKAVLELVMMQOTAFIKAKSHDFIG-----YVFER 260
257 GNTLGVL---VDPLLV-----RDEORS-----S 277
261 -NVLATVAYVNDNLGNQVFEPLPODEKEVESALVTFIHYHSTNKKIKPTLVLS 319
278 ESNMLLP-----PFIQPKPIVITPIRPSAHMDVFLKDIFGPEGVYETRI 329
320 EENLSLANSKINVTQPK-NGEOKSILQTVI-----DNARYALNTKW 361
330 LPLIGNIKAPQVPICTMGTVLETLFYKGDPEDEPEISGDDGVNLVSLALAS 389
362 TGFNNLNRAEVHQLLOLQVPSIQSL-----EIIDISFYDKDVVG-----A 405
390 LMKENKQYLVK-----VKIDGVSHTSILKDEVALNEIVGETTSINSHAEGLSNL 440
406 MLRYENGKMKALSRRYNNINIDHKGDTNYMAD-VVYRRI---ISSIQTHKOLPLSDL 458

RESULT 13
ESTS_DROVI STANDARD: PRT: 542 AA.
ID 005487:
AC 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Esterase S precursor (EC 3.1.1.1) (EST-S) (Carboxylic-ester hydrolase).
GN ESTS.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93347990; PubMed=8346032;
RA Sergeev P.V., Yenikolopov G.N., Penouva N.I., Kuzin B.A., Khechumian R.A., Korochokin L.I., Georgiev G.P.;
RT "Regulation of tissue-specific expression of the esterase S gene in Drosophila virilis";
RL Nucleic Acids Res. 21:3545-3551(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392127; PubMed=2783177;
RA Sergeev P.V., Castillo J.E., Penouva N.I., Yenikolopov G.N.;
RT "Primary structure of the esterase S gene from Drosophila virilis.";
RL Bloorg. Khim. 15:839-843(1989).
CC -1- FUNCTION: TRANSFERRED FROM THE EJACULATORY BUBBS OF MALES TO THE FEMALE GENITALS UPON COPULATION, PLAYS AN IMPORTANT ROLE IN THE REPRODUCTIVE BIOLOGY.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O - an alcohol + a carboxylic anion.
CC -1- SUBUNIT: MONOMER.
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN THE EJACULATORY BUBBS OF MALE.
CC -1- DEVELOPMENTAL STAGE: IN THE MALE, IT APPEARS 3 DAYS AFTER EMERGENCE IN THE IMAGO STAGE AND REACHES MAXIMUM LEVELS BY THE 10TH DAY.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
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CC -----
CC EMBL: X70351; CAA49809.1; -.
CC PIR: J00438; J00438.
CC PIR: S32019; S32019.
CC PIR: S34853; S34853.
CC HSSP: P21836; IMAA.
CC FlyBase: FBgn0013077; Dvir\Ests.
CC InterPro: IPR002018; Carbesteraseh.
CC Pfam: PF00135; Coesterase; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_B_1; 1.
CC KW Hydroxylase; Serine esterase; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 542
FT ACT_SITE 204 204 BY SIMILARITY.
FT DISULFID 81 100 BY SIMILARITY.
FT DISULFID 256 268 BY SIMILARITY.
FT DISULFID 507 528 POTENTIAL.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 542 AA; 61069 MW; 9134648A7B573F84 CRC64;

Query Match 4.4%; Score 102; DB 1; Length 542;
Best Local Similarity 20.8%; Pred. No. 1.6;
Matches 106; Conservative 75; Mismatches 170; Indels 158; Gaps 26;

QY 18 VVVVVVMSLICTGASNL-DPLLIPGNGQLARLNLQKPSFICESVPL-----I 72
DB 1 MQLILPLALLCLFPASTLSNPLVLELPG--ELNGRNGFYSTESIPVAPPIDICL 58
QY 73 KKNKGWFLMPSDYSILAFPTQCFARMTLHYHOELDDYFNTPGVETRVPHGGSNSLY 132
DB 59 EEPRTYERWENTFDATRPVDCI-----QMSOLISQPNKLT-----GSDELTLV 103
QY 133 LNPRLKHITGYAPLVDSIQKIGYADGETLGAPVD-----FRY 171
DB 104 STYKPKNLIRISFPVVAHIFGGWS-----FGAALDDGVRPSSGNYIVKTTTEWERL 158
QY 172 GLAAGHPGSOVSKFLDKNLIIEASNS--NNGKP--VILSHSLGGLV-IQLNRN 225
DB 159 GFMSTGDSYIPGNFGKLDRLAIKIRNNIARFGSDPINIILGFGSTGSSVHDLMKKE 218
QY 226 PPSMKRKFIFKFIASL---APW---GGAIDEMTYFASGNTLGVLPVLLVLD-----E 273
DB 219 ---YGLYKKAISISGATVMAVQANARD--LAFRYGKLLGCN--NPKNSRELKDCOLK 270
QY 274 QRSSESNMLLPNKI-----FGPKPIVITPIRPSAHMDVFLKDIFGPEGVYETRI 328
DB 271 KTDAAEFVSTLNLQVFDVVPFGPGPVVES-----PEVESPLVLT- 310
QY 329 ILPLGNIKAPQVPICTMGTVLETLFYKGDPEDEPEISGDDGVNLVSLALAS 386
DB 311 -----ELPDTIR-----SGFAQVPMWLASTTPENGILYNAALLAK 346
QY 387 -----IQLMKKE-----EKNQYLVKID--GVSHSTILK-----D 415
DB 347 DANGKERIEELNTRNRELAPYFLAYPTLKSENMAHQKLYQLGKKNSSVNYVPDYQ 406
QY 416 EYALNEIV--GETTSINSHAEIGLSNLF 442
DB 407 RLFTNELYKKGIELSLDSHRKHGASPVYA 435

RESULT 14
Y4KF_RHISN STANDARD: PRT: 434 AA.
ID Y4KF_RHISN
AC P55526;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 47.4 kDa protein Y4KF.
GN Y4KF.

```

OS Rhizobium sp. (strain NGR234).
OC Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -1- SIMILARITY: NONE OBVIOUS.
CC -----
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CC -----
CC EMBL, AE000081; AB91737.1;
DR InterPro; IPR00379; Set-estrs-site.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 434 AA; 47425 MW; BA0FCCE3B2E494B CRC64;

Query Match 4.3%; Score 99.5; DB 1; Length 434;
Best Local Similarity 21.5%; Pred. No. 1.9;
Matches 50; Conservative 41; Mismatches 77; Indels 65; Gaps 12;

OY 115 PGEVRVPHFGSTNSLILYINPRLKHTGYMAPLVDSLOKIGYADGTELEGAPYDFRYGLA 174
DB 173 PADKKLETFG-----LSGMLASTKELALGASAPADATTA-----GLL 211
OY 175 AEGHPS--QVSGKFLKD---LKN-----LIE-----EASNSNNGKPYLLS 210
DB 212 ALGRSASAHQKASRFLGDVYVLYLNKRTAAAPPIYRAVLQAFRNDAARQEGDDKLITVG 271
OY 211 HSLGGLFVQLIDNRPSPRRKFKIKHFLASAPWGAIIDEMTFASGNLGLVPLVPLV 270
DB 272 HSLGGVITYDIILSYRAPDLK---VDYLATIGSQVGLFDEMLIYSRPLPPGMP-TDP--- 323
OY 271 RDEORSSSENLT--WLLPNPKIFGPOKPIYITPIRPSAHDMVDFLKDIFGPEG 321
DB 324 KNDRIANPNVGKML---NVFD-----TNDVFSSASAGIYKSVADPQYDYG 366

RESULT 15
ETFL_FOMPV STANDARD; PRT; 633 AA.
AC P21966; O9J5F2;
DT 01-AUG-1991 (Rel. 19, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Early transcription factor 70 kDa subunit (VETf small subunit).
GN FPOV057 OR FPOD6.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90324937; PubMed=2165135;
RA Tartaigla J., Winslow J., Goebel S., Johnson G.P., Taylor J.,
RA Paoletti E.;
RT "Nucleotide sequence analysis of a 10.5 kbp HindIII fragment of
RT fowlpox virus: relatedness to the central portion of the vaccinia
RT virus HindIII D region.";
RL J. Gen. Virol. 71:1517-1524(1990).
RN [2]
RP SEQUENCE FROM N.A.

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RX MEDLINE=20193820; PubMed=10729156;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
CC -1- FUNCTION: ACTS WITH RNA POLYMERASE TO INITIATE TRANSCRIPTION FROM
CC EARLY GENE PROMOTERS. A DNA-DEPENDENT APPASE ACTIVITY IS
CC ASSOCIATED WITH VETf.
CC -1- SUBUNIT: HETERODIMER OF A 70 kDa AND A 82 kDa SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE VETf SUBFAMILY OF HELICASES.
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CC -----
CC EMBL, X17202; CA35069.1;
DR EMBL; AF198100; AAF4401.1;
DR PIR; F35216; F35216.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002464; DEAD_Box.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00690; DEAD_ATP_HELICASE; 1.
KW Helicase; Transcription regulation; Activator; ATP-binding.
FT NP_BIND 45
FT SITE 135 138 DEAH BOX.
FT FT CONFLICT 605 633
FT REF. 1).
SQ SEQUENCE 633 AA; 73020 MW; C17DE6A97EBEAD25 CRC64;

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Query Match 4.2%; Score 99; DB 1; Length 633;
Best Local Similarity 20.7%; Pred. No. 3.4;
Matches 89; Conservative 58; Mismatches 144; Indels 138; Gaps 23;

OY 71 LIRKKNQWRLMFDDSVIIAPFTQCAEEMTLHYHELDYFNTPEVERVPHFGSTNSL 130
DB 215 ILNKKISTYEL-----CDELPSTIFHK--EFLDTKYVYCKMSKLOETD-- 257
OY 131 LYINPRL-----KHIT-----GYMAP--LYVDSLOKIGYADGETLF-----GAPYDF 169
DB 258 -YINVRKLCNNEMFEKNMNVSLAVGLPLNANSLELLEVEQDKELYPLKINDGVLY-- 314
OY 170 RIGLAEGHPQVSGKFLKDLKNLIEASNSNNGKPYILLSHS-LGGLFVQLIDNRPN--- 225
DB 315 ---GDELTKLNISKF---KYFIDTIGNL-TGKNFIYFSNSTYGLVIKYIMLNNGYS 365
OY 226 -----PPSWKRRKFKIKHFLASAPWGAIID---EMYTFASGNITGLVPLVPLVRDQ 274
DB 366 EYASOGQINPKMINKHLKTFALVTSKMSKSLLELVYN-SPENDNGEKI---WFLPSSN 421
OY 275 RSSES-----NLMLLPNKIFGPOKPIYITPIRPSAHDMVDFLKDIFGPEGYPER 327
DB 422 IMSESTLIKEVRNIMWMTIPDFSQYNQILGRIRFS-----YKDVSKPYNRY--- 470
OY 328 RILPLIGNIKAP-QVPIYICMGTVGTLTFLYEGKDDPDERPEISYGGDGGVYVNLVSLA 386
DB 471 ---LLATVYSPENDTITSIDYSIDINTL-----PFD-----IKLLY 506
OY 387 LOSLWKEEKNQYLYKVIDGVSHTSLTK-----EVALNEIYGEITSINSH 432
DB 507 LKFKTKETKRIY-----STLKDLSTINRSPHPHYITDVVGLGVROFFYHNSR 554
OY 433 AELGLSNLF 441
DB 555 VSINDAKLF 563

Search completed: February 11, 2003, 19:14:37
Job time : 17 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 19:12:56 : Search time 35 Seconds
(without alignments)
2607.968 Million cell updates/sec

Title: US-09-857-612A-14
2333
Perfect score: 1 MKRQEGSLKIEVATLTIVT.....GEISINSHELGLSNLEFSG 443
Sequence:

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1380.5	59.2	432	10 Q9FZ18	Q9FZ18 arabidopsis
2	831	35.6	822	10 Q8S5X5	Q8S5X5 oryza sativ
3	792.5	34.0	266	10 Q9SDR9	Q9SDR9 prunus dulc
4	673.5	28.9	363	10 Q8RYV9	Q8RYV9 oryza sativ
5	612	26.2	412	11 Q8VER4	Q8VER4 mus musculu
6	610	26.1	412	4 Q9Y2B3	Q9Y2B3 homo sapien
7	586	25.1	407	6 Q8WMP9	Q8WMP9 bos taurus
8	570	24.4	421	5 Q9Y168	Q9Y168 drosophila
9	560	24.0	421	5 Q9Y179	Q9Y179 drosophila
10	546	23.4	440	6 Q9MZ04	Q9MZ04 tupaia glis
11	533.5	22.9	451	13 Q9DDJ6	Q9DDJ6 anas platyr
12	526	22.5	440	11 Q35849	Q35849 ratus norv
13	518	22.0	444	11 Q9CW47	Q9CW47 mus musculu
14	512.5	22.0	417	5 Q21515	Q21515 caenorhabdi
15	457.5	19.6	272	4 Q9UG04	Q9UG04 homo sapien
16	436.5	18.7	443	10 Q94HP5	Q94HP5 oryza sativ

17	369.5	15.8	298	11 Q35726	Q35726 marmota mar
18	364	15.6	307	11 Q35503	Q35503 cricetus
19	351.5	15.1	291	11 Q35746	Q35746 spalax leuc
20	351	15.0	295	11 Q35574	Q35574 gerbillus h
21	342	14.7	294	11 Q54727	Q54727 akodon torq
22	340	14.6	297	11 Q35591	Q35591 myoxus glis
23	336	14.4	296	11 Q35747	Q35747 nanospalax
24	331	14.2	292	11 Q35839	Q35839 sciurus gril
25	329.5	14.1	274	11 Q35580	Q35580 myocastor c
26	325.5	14.0	268	11 Q9EP22	Q9EP22 dipus sagit
27	323.5	13.9	268	11 Q9EP6	Q9EP6 allactaga e
28	322.5	13.8	268	11 Q9EP5	Q9EP5 calomyscus
29	319.5	13.7	268	11 Q9EP0	Q9EP0 phodopus ro
30	317.5	13.6	272	11 Q35830	Q35830 rhizomys pr
31	315.5	13.5	268	11 Q9EP9	Q9EP9 lophuromys
32	314.5	13.5	267	11 Q9EP0	Q9EP0 jaculus jac
33	311.5	13.4	268	11 Q9EP8	Q9EP8 mystromys a
34	307	13.2	256	11 Q9EPC9	Q9EPC9 sicista kaz
35	305.5	13.1	268	11 Q9EP3	Q9EP3 dendromys m
36	304.5	13.1	268	11 Q9EP4	Q9EP4 neotoma fus
37	301.5	12.9	268	11 Q9EP3	Q9EP3 napaeozapus
38	300.5	12.9	192	4 Q9NP06	Q9NP06 homo sapien
39	299.5	12.8	268	11 Q9EP1	Q9EP1 dicystomys
40	299.5	12.8	268	11 Q91YH4	Q91YH4 cricetomys
41	298.5	12.8	265	11 Q91YB3	Q91YB3 sacostomus
42	295.5	12.7	264	11 Q9EP6	Q9EP6 macrotarom
43	295.5	12.7	268	11 Q9EP5	Q9EP5 myospalax s
44	294.5	12.6	268	11 Q9EP2	Q9EP2 nesomys rui
45	285.5	12.2	266	11 Q9EPC8	Q9EPC8 steatomys s

ALIGNMENTS

RESULT 1					
Q9FZ18	PRELIMINARY;	PRT;	432 AA.		
AC Q9FZ18:					
DT 01-MAR-2001 (TREMBLrel. 16, Created)					
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)					
DE F17L21.27 (ATIG27480/F17L21_28).					
OS Arabidopsis thaliana (Mouse-ear cress).					
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:					
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;					
OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.					
OX NCBI_TaxID=3702;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,					
RA Shinn P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,					
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,					
RA Lenz C., Li J., Liu J., Liu K., Liu S., Mukharzky N., Nguyen M.,					
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,					
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,					
RA Ecker J.R.;					
RT "Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome					
RT I."					
RT Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.					
[2]					
RP SEQUENCE FROM N.A.					
RA Ecker J.R.;					
RP Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.					
[3]					
RP SEQUENCE FROM N.A.					
RA Ecker J.R.;					
RP Submitted (Jun-1998) to the EMBL/Genbank/DBJ databases.					
[4]					
RP SEQUENCE FROM N.A.					
RA Ecker J.R.;					
RP Submitted (Dec-1998) to the EMBL/Genbank/DBJ databases.					
[5]					
RP SEQUENCE FROM N.A.					

RA Ecker J.R.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altai H., Bei B., Chin C., Chlou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharasy N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaverl A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
 RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamly A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC004557; AA99739.1; -;
 DR EMBL; AF367336; AA32913.1; -;
 DR InterPro: IPR003386; LACT.
 DR InterPro: IPR003379; Ser_estrs_site.
 DR Pfam: PF02450; LACT.1.
 SO SEQUENCE 432 AA; 48307 MW; 4ACD9608C6785078 CRC64;

Query Match 59.2%; Score 1380.5; DB 10; Length 432;
 Best Local Similarity 61.0%; Pred. No. 1.7e-11;
 Matches 264; Conservative 62; Mismatches 92; Indels 15; Gaps 5;

QY 1 MKKDEESLKEVAVLTVTVVVVM..SLCTCGASVLDPLILIPGNGQLBARLTNOYKP 60
 DB 1 MKK-----ISSHYSVVIALIVVTMTSMCAVGSNVYPLILVPGNGQLREYKRP 55
 QY 61 STFCESW-YPLIKKKNMFRLMFDSSVILAPFTQCFERMTLHYHQELDVFNTPGVET 119
 DB 56 SSVWCSSWLYPIHKKSGCMFLMFDPAVALLSPFTRCFSDRMALYDPLDDYQNAFGVOT 115
 QY 120 RVPHFGSTNSLLYLNPRILKHTGYAPLVDSLO-KLGYADEGTEFGARYDRYGLAAGH 178
 DB 116 RVPHFGSTKSLLYLDRPILRDATSYEMHLVKALEKCGVNDOTILGAYDRYGLAAGH 175
 QY 179 PSQVSGSKFLDKLNLIEEASNSNNGKPYILLSHSLGSLFVLOLNRPNSRRKFKIKFI 238
 DB 176 PSRAVSGFLQDLKQLEVTSSSENEKRPYILLSHSLGSLFVLLHFLNRTTPSMRRKTIKAFV 235
 QY 239 ALSAPMGALIDEMVTFASGNTLGVPLVLDPLVDRDQSSSESNLMLPNPKIFGPO-KPIV 297
 DB 236 ALAAPMGGTISQMKTFASGNTLGVPLVPLVRRHQRTSESNOMLPTSTVFHDBRTKLV 295
 QY 298 ITPRPYSAHOMVDFLAKIGFPEGVYPTETRIPLIGINAKAPOVPTICMGVGTLETL 357
 DB 296 VTPQVNTAYVEMDRFADIGFSQGVAPYKTRVPLPLELMLPMPGVAVTCIYGRGVDTPEVL 355
 QY 358 FYGKGDPERPEISGDDGTVNLVSLALQSLMKEEKNOYLKVKYKIDGVSHTSLKDEY 417
 DB 356 MYGKGGEKPEIKYGGDDGTVNLASLAL-----KVDSLNTVEIDGVSHSTSLKDEI 408
 QY 418 ALNEIVGEITSIN 430
 DB 409 ALKEIMQISTIN 421

RESULT 2
 ID 0853X5 PRELIMINARY; PRT; 822 AA.
 AC 0853X5;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 91.2 kDa protein.
 GN O0175C11.13.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzaeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
 RA Saeki C., Henry D., Oates R., Simmons J.;
 RT "Rice Genomic Sequence";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC103891; AAM19133.1; -;
 KW Hypothetical protein.
 SO SEQUENCE 822 AA; 91220 MW; 8F329D21E6232ABE CRC64;

Query Match 35.6%; Score 831; DB 10; Length 822;
 Best Local Similarity 42.2%; Pred. No. 2.8e-63;
 Matches 183; Conservative 70; Mismatches 151; Indels 30; Gaps 10;

QY 18 VTVVVVMSL-----LTCGASNDPLILIPGNGQLBARLTNOYKSTFCESWYPLIK 73
 DB 395 VAVVAVLILSLPSRSGSGGSDLHPVYLPDYGSNRLYARLTAAVEPAAPRCG----RE 450
 QY 74 KKNQMFRLM-FDSSVILAPFTQCFERMTLHYHQELDVFNTPGVETRVPHFGSTNSLLY 132
 DB 451 GKDEMFQLPIDAAASEPAQAPCLAEMKSLYDPAVDYDRVAVAGVYRVPSFASTRALV- 509
 QY 133 LNPRLKHTGYMAPLVDSLOKLGYADEGTEFGARYDRYGLAAGHPSQVSKFLDKLN 192
 DB 510 -----GW-DPLVQLLEAMGHRDGSGLPAAYDRYAVAPAPGHPSAVGERFARLTR 559
 QY 193 LIEEASNSNNGKPYILLSHSLGSLFVLOLNRPNSRRKFKIKFIKLSAPMGALIDEMV 252
 DB 560 LIEEASRLNGRPVAVVAHSFGALTYOFLARPLARORVKAVALLAALGSGFAGMD 619
 QY 253 TFASGNTLGVPLVLDPLVDRDQSSSESNLMLPNPKIFGPOKPIVTPRPYSAHMVDV 312
 DB 620 GLASGAGSGPLNLPAPARARLARSQSLWRLPVMFG-DRPVVVKNSYANNITEF 678
 QY 313 LKDIGFPEGVYPTETRIPLIGINAKAPOVPTICMGVGTLETLFGKGDPERPEISY 372
 DB 679 LDAIGTEGVQPYTRVLPMPMRALPAPVPTSMYGVGRTPETFGVGEAGFEGTPEVY 738
 QY 373 GDGQGTNVSLVSLALQSLMKEEKNOYLKVKYKIDGVSHTSLKDEVALNEIVGEI---TS 428
 DB 739 GDGQGNMNIYSLMAAE-WSGVEQIILKVVRLPGVSHVGFPSD-LALKVYAEIQKAVSS 796
 QY 429 INSHAELGLSNLFS 442
 DB 797 IEVHRK---EKIFS 807

RESULT 3
 ID 09SDR9 PRELIMINARY; PRT; 266 AA.
 AC 09SDR9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Lecithin-cholesterol acyl transferase (Fragment).
 GN LCAT1.
 OS Prunus dulcis (Almond) (Prunus amygdalus).
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotys; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=3755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BOA CASTA;
 RA Ma R.C., Oliveira M.M.;


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      240 LASDNNRIPVIGPKTRRQORSASVSTSWLLPYNHTWSHEKVFYPTNTNLTDRYHRNF 299
      314 KDIFPEGVVPEYTRILPLINIKAPQVPTICMGVTGLETLEFYGKGDDEDER-PEISY 372
      300 RDIPEEGWFMKROD-TEGLVFAKMPFGVCLHCLGTGTGPTNSRY--ESPDPDRKICF 356
      373 GDSGTYNVLVSLALQSLMKKEKNQYLKVKRIDGVSHTSILKDEVAL 419
      357 GDSGTYNVLVSLALQSLMKKEKNQYLKVKRIDGVSHTSILKDEVAL 402

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RESULT 6

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      09Y2B3 PRELIMINARY; PRT; 412 AA.
      AC 09Y2B3;
      DT 01-NOV-1999 (Tremblrel. 12, Created)
      DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
      DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
      DE LCAT-like lysophospholipase (LPL).
      OS Homo sapiens (Human).
      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
      OX NCBI_Taxid=9606;
      RN [1]
      RP SEQUENCE FROM N.A.
      RX MEDLINE=9914552; Pubmed=10092508;
      RA Tanigawa Y., Shibata S., Kita S., Horikoshi K., Shirafuji H.,
      RA Sumino Y., Fujino M.;
      RT "Cloning and expression of a novel lysophospholipase which
      RT structurally resembles lecithin cholesterol acyltransferase."
      RL Biochem. Biophys. Res. Commun. 257:50-56(1999).
      DR EMBL: AB017494; BAA76877.1; -.
      DR InterPro: IPR003386; LACT.
      DR Pfam: PF02450; LACT; 1.
      SO SEQUENCE 412 AA; 46657 MW; 1FEA8A5783AF050A CRC64;

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Query Match 26.1% Score 610; DB 4; Length 412;

Best Local Similarity 34.8%; Pred. No. 1.6e-44;

Matches 141; Conservative 80; Mismatches 156; Indels 28; Gaps 12;

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      21 VVWVLSLLC--TCGASNDPLILIPGNGNQLRLTNOYKRPST--FICESMYPLIKKN 76
      20 LLLMLLADBALPAGKRPVVLVPGDLGNLEKLD---KPIVHYLCS-----KTE 70
      77 GMPRLWDSSVILAPFTQCAERMTLHYHOELDYFNTPEVETRVPHFGSTNSLLYNPR 136
      71 SYFTIMNLELLPVIIDCWNIDNIRLVYNTKTSRATQPPDGDVAVPGEGKFFSLEFLDPS 130
      137 LKHITGMAPLVDSLQGLGADGETLPGAPYDFRYGLAEGHPSQVSKFLDKNLIEE 196
      131 KSSVGSYFHTWVESLVGMGYTRGEDVAGAPDWRRA-----PNENGPYFLA-LREIMEE 183
      197 ASNSNGKPYILSHSLGGLFVLOLNRNPPSWMKKFKIKHIALSAPMGALIDMYFFAS 256
      184 MYQLYGS-PVYLVANSHGNNMTLYFLQROPOAMKDKITRAVFSGAGWGVAKTLRVLAS 242
      257 GNTLGVPLVDPFLVDRORSSESNTMLLPNKITFGPKPIVPIPIRYSAHDWVFLDKI 316
      243 GDNRRIVIVIGPKTRRQORSASVSTSWLLPYNHTWSPEKVVQPTTYTLTRDYKFFODI 302
      317 GEPFG-VVPEYTRILPLINIKAPQVPTICMGVTGLETLEFYGKGDDEDER-PEISYGD 374
      303 GFEDGWLMDRDE--GLVEATMPGVOHLCLYGVPTPSFVY--ESFPDRDKICFGD 358
      375 GDSGTYNVLVSLALQSLMKKEKNQYLKVKRIDGVSHTSILKDEVAL 419
      359 GDSGTYNVLVSLALQSLMKKEKNQYLKVKRIDGVSHTSILKDEVAL 402

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      08WMP9 PRELIMINARY; PRT; 407 AA.
      ID 08WMP9

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      AC 08WMP9;
      DT 01-MAR-2002 (Tremblrel. 20, Created)
      DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
      DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
      DE Lysosomal phospholipase A2.
      GN LPLA2.
      OS Bos taurus (Bovine).
      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
      OC Bovidae; Bovinae; Bos.
      OX NCBI_Taxid=9913;
      RN [1]
      RP SEQUENCE FROM N.A.
      RA Hiraoaka M., Abe A., Shayanman J.A.;
      RT "Cloning and characterization of a lysosomal phospholipase A2, 1-O-
      RT acylceramide synthase."
      RL J. Biol. Chem. 0:0-0(2002).
      DR EMBL: AY072914; AAL65270.1; -.
      DR InterPro: IPR003386; LACT.
      DR Pfam: PF02450; LACT; 1.
      SO SEQUENCE 407 AA; 46062 MW; CEASAB747E7EB8FC CRC64;

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Query Match 25.1% Score 586; DB 6; Length 407;

Best Local Similarity 35.1%; Pred. No. 1.9e-42;

Matches 137; Conservative 72; Mismatches 157; Indels 24; Gaps 10;

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      33 ASNDPLILIPGNGNQLRLTNOYKRPST--FICESMYPLIKKNCFRLMFDSSVILA 90
      29 AGSRPVLVPGDMGNLEKLD---KPSVHYLCS-----KRTDYFTLMNLELLP 79
      91 PFTQCAERMTLHYHOELDYFNTPEVETRVPHFGSTNSLLYNLPLKHTITGMAPLVDS 150
      80 VIIDCWNIDNIRLVYNTKTSRATQPPDGDVAVPGEGKFFSLEFLDPSKSSVGSYLHTWVES 139
      151 LQKLYADGETLPGAPYDFRYGLAEGHPSQVSKFLDKNLIEESNSNMGKPYILS 210
      140 LVSWGYTRGKDYAGAPDWRRA-----PNENGPYFLA-LKMLEEYQLYGS-PVYLV 191
      211 HSLGGLFVLOLNRNPPSWMKKFKIKHIALSAPMGALIDMYFFASGNTLGVPLVDPFLV 270
      192 HSMGNMYMLVFLQHPQDMKDYIRAVVAGPMPGVPTKTLRVLASDNNRIPVIRSLKI 251
      271 RDEORSSESNTMLLPNKITFGPKPIVPIPIRYSAHDWVFLDKIDFEPGCVPEYTRIL 330
      252 RAQORSASVSTSWLLPYSTWSPQKVFVETRPKANVTLDYQFQFODIGFKDG-MSMRDTE 310
      331 PLGINIKAPQVPTICMGVTGLETLEFYGKGDDEDER-PEISYGDGTYNVLVSLALQSL 389
      311 GLVEATVPPGVRLHCLGTGTGPTPSFVY--ESFPDRDKIHYGDSGTYNVLVSLALCHT 368
      390 LMKKEKNQYLKVKRIDGVSHTSILKDEVAL 419
      369 -WRGLQKQEVSLQALPENGHIAMLANNTTL 397

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RESULT 8

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      09Y168 PRELIMINARY; PRT; 421 AA.
      AC 09Y168;
      DT 01-NOV-1999 (Tremblrel. 12, Created)
      DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
      DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
      DE BCDNA.GH02384.
      GN BCDNA:GH02384 OR CG18858.
      OS Drosophila melanogaster (Fruit fly).
      OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
      OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
      OC Ephyridioidea; Drosophilidae; Drosophila.
      OX NCBI_Taxid=7227;
      RN [1]
      RP SEQUENCE FROM N.A.
      RA Rudin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
      RA Agbayanl A., Arcaina T.T., Baxter E., Blazek R.G., Butenhoff C.,

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QY 38 P L I L I P G N G N O L E A R L T N O Y K R S T - T F I C E S M Y P L I K K K N G M F R L M P D S S V I L A P T Q C 95
D B 48 P V I L V P G C G N R L E A K L D - - - K P N V Y N W L C - - - - - Y R K T E D F F T I W D F N L F P L G V D C 98
QY 96 F A E R M T L H Y H O E L D Y F N T P G V E T R Y P H G S T N S L Y L N P R L K H T I G Y A P L V D S I O K I G 155
D B 99 W I D N T R V Y V N R S S G H M S N A P G V O I R N P G R K T Y S E Y E I D D - - N K L A G I L H T L V O N L V N N G 156
QY 156 Y A D G E T L G A P Y D F R Y G L A E G H P S O V S K F L K D K N L I E E A S N S N G K P V I L L S H S I G G 215
D B 157 Y R D E T V R A A P Y D W R L A - - - - - P R O - O D E Y Y K K L A G I V E E - M Y A A Y K P V F L I G H S I G C 208
QY 216 L F V L O L N R P P S R K K F I K H F I A L S A P W G A I D E M T P F A S G N T L G V P L V D P L V D E R 275
D B 209 L H V L H F L R O P S W K D H F I D G F I S L G A P W G S I K P R I L A S G D N O G I P L M S N I K L E E O R 268
QY 276 S E S N L M L P N P K I R G P Q P I Y T P I R P Y S A H D W D F L K D I G F P E G Y P Y - E T R I L P L I G N I 334
D B 269 I T T S P M L P A P H W P E D H V F I S T P N F N Y T G D P E R F F A D L H F E B G M H F I Q S R - D L L A 326
QY 335 N I K A P O V P T I C I M G T G V L E T L F Y G K G D F D E R P E I S - - Y D G D G T V N L V S L A L O S L M K 392
D B 327 G L P A G V E Y C L Y G V G M P F A H T Y I Y D H - N F P Y K D P V A L Y E D G D D V A T R S - T E L C G O M Q R 384
QY 393 E E K N O Y L K V K I D G V S H T S I L K D E V A L N E I 422
D B 385 G R O S A V H L P M N G T D H L M V F S N K T L E H I 414

RESULT 13
Q9CM47 PRELIMINARY: PRT: 444 AA.
AC Q9CM47:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Lecithin cholesterol acyltransferase (Fragment).
GN LCAT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuell P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitteker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
DR EMBL: AK004914; BAB23665.1; -.
DR MGD; MGI:96755; Lcat.
DR InterPro; IPR003386; LACT.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02450; LACT; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
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FT NON_TER 1 1
SQ SEQUENCE 444 AA: 50535 MW: 7936970447639A63 CRC64;
Query Match
Best Local Similarity 33.2%; Score 518; DB 11; Length 444;
Matches 129; Conservative 71; Mismatches 164; Indels 24; Gaps 12;
QY 38 P L I L I P G N G N O L E A R L T N O Y K R S T I C S M Y P L I K K K G M F R L M P D S S V I L A P T Q C R A 97
D B 54 P V I L V P G C G N R L E A K L D - - - K P D V Y - - - N M M - C Y R K T E D F F T I W D F N L F P L G V D C W I 106
QY 98 E R M T L H Y H O E L D Y F N T P G V E T R Y P H G S T N S L Y L N P R L K H T I G Y A P L V D S I O K I G Y A 157
D B 107 D N T R I Y V N N S S G R V S N A P G V O I R N P G R K T Y S E Y E Y D D - - N K L A G I L H T L V O N L V N N G T V 164
QY 158 Y A D G E T L G A P Y D F R Y G L A E G H P S O V S K F L K D K N L I E E A S N S N G K P V I L L S H S I G L F 217
D B 165 R D E T V R A A P Y D W R L A - - - - - P H Q - O D E Y Y K K L A G I V E E - M Y A A Y K P V F L I G H S I G C L H 216
QY 218 V I O L N R N P P S R K K F I K H F I A L S A P W G A I D E M T P F A S G N T L G V P L V D P L V D E R O R S 277
D B 217 V H F L R O P S W K D H F I D G F I S L G A P W G S I K A M R I L A S G D N O G I P L S N I K L E E O R Y T 276
QY 278 E S N L M L P N P K I R G P Q P I Y T P I R P Y S A H D W D F L K D I G F P E G Y P Y - E T R I L P L I G N I 336
D B 277 T T S P M L P A P H W P E D H V F I S T P N F N Y T G D P E R F F T D L H F E B G M H F I Q S R - D L L E R L 334
QY 337 K A P O V P T I C I M G T G V L E T L F Y G K G D F D E R P E I S - - Y D G D G T V N L V S L A L O S L M K E E 394
D B 335 P A P G V E Y C L Y G V G R P T P H T Y I Y D H - N F P Y K D P V A L Y E D G D D V A T R S - T E L C G O M Q R 392
QY 395 K N O Y L K V K I D G V S H T S I L K D E V A L N E I 422
D B 393 Q S Q P V H L P M N E T D H L M V F S N K T L E H I 420

RESULT 14
Q21515 PRELIMINARY: PRT: 417 AA.
AC Q21515:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE M05B5.4 protein.
GN M05B5.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RA Gardner A.E.;
RN Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z71265; CAA95883.1; -.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR003386; LACT.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02450; LACT; 1.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
SQ SEQUENCE 417 AA: 46839 MW: EBBB0F403F9053B CRC64;
Query Match
Best Local Similarity 32.8%; Score 512.5; DB 5; Length 417;
Matches 129; Conservative 79; Mismatches 160; Indels 25; Gaps 12;
QY 38 P L I L I P G N G N O L E A R L T N O Y K R S T - T F I C E S M Y P L I K K K N G M F R L M P D S S V I L A P T Q C 95
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Db 35 PVLIVGGGGSGQLESNLIG--KPSVHYVCS-----KOTADYFOLMLNLQLETPPLVIDC 86
QY 96 FAERMTLHYHOELDDYFNTPGVETRVPHFGSTNSLLYLNPRLKHTIGYMAPLVDSLOKLG 155
Db 87 WADNNQVLFNTTGTGSEMMPGVDIVAGFGATESVEMWDKSAASGRFFPDIVDSMSWG 146
QY 156 YADGETLFGAPYDFERYGLAEGHPQVSGSKFLDKNLIEEASNSNNGKPVILLSHSLGG 215
Db 147 YRRGNVIGAPDFDMRS-----PNEL-NDYLIQLKSLIETTYRWNDQKIYLVHSGN 199
QY 216 LFLVQLLNRN-PPSWRRKFIFKFIILSAPWGAIDEMTFASGNTLGV--PLVDDLARD 272
Db 200 PLSLFLNNYVDQAKDKYISSFVSLAPWAGSMQIVRLFASGYNMNYRVILPPSSLRA 259
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Db 319 NGNLSSPGVPVHCIGVTPPEKFSMAQYFPDYPTEFGDGDGTVKKKSATVCTN-W 377
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RESULT 15

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DT 01-MAY-2000 (TREMBLrel.13, Created)
DT 01-MAY-2000 (TREMBLrel.13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel.19, Last annotation update)
DE Hypothetical 31.0 kDa protein (unknown) (Protein for MCC:12657).
CN DKFZP564A0122.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL110209; CAB53675.1; -.
DR InterPro: IPR003386; LACT.
DR Pfam; PF02450; LACT; 1.
KW Hypothetical protein.
SQ
SEQUENCE 272 AA; 31016 MW; ACCC5E1680D7A720 CRC64;

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Query Match 19.6%; Score 457.5; DB 4; Length 272;
 Best Local Similarity 37.1%; Pred. No. 1.6e-31;
 Matches 102; Conservative 54; Mismatches 104; Indels 15; Gaps 8;

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QY 207 ILSHSLUGLFLVQLNLNPNPSMRKKFKHFIASAPWGAIIDENYTFASGNTLGVPLVD 266
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QY 267 PLVVRDEORSESNLMLPNPKIGPOKPIVITPIRPSAHDMDFLKIDGPEGVYPER 325
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QY 385 LALQSLMKEENQYLYKVKIDGVSHTSILKDEVAL 419
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Search completed: February 11, 2003, 19:15:18
 Job time : 37 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 15, 2003, 13:17:02 : Search time 2485 seconds

(without alignments)
5188.146 Million cell updates/sec

Title: US-09-857-612a-14
Perfect score: 2333
Sequence: 1 MKKEDEGKIEVATLVTV.....GETTSINSHALGLSNLFG 443

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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40: em_htgo_mus : *
41: em_htgo_other : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1380.5	59.2	1457	8	AF367326 Arabidops
4	1380.5	59.2	1498	8	AY087433 Arabidops
5	1310	56.2	1362	6	AX037586 Sequence
6	1310	56.2	1562	6	AX037605 Sequence
7	1310	56.2	99690	8	AC004557 Genomic s
8	1174	50.3	134188	2	AC120983 Oryza sat
9	900	38.6	833	8	AF209909 prunus du
10	696.5	29.9	123620	8	AC103891 Oryza sat
11	675	28.9	139534	2	AF005640 Oryza sat
12	655.5	28.1	147548	8	AP004073 Oryza sat
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21	606	26.0	1137	6	E26768 Novel prote
22	601	25.8	2722	9	HSMB00863 Novel prote
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24	594	25.5	1233	6	E26767 Novel prote
25	594	25.5	1242	6	E26770 Novel prote
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28	554	23.7	1135	6	AX090327 Sequence
29	546	23.4	1338	4	AF272861 Tupai gl
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33	541	23.2	1360	9	BC014781 Homo sapi
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37	541	23.2	4308	6	AX077320 Sequence
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45	516	22.1	1341	10	MUSLCATX J05154 Murine choi

RESULT 1

ALIGNMENTS

TITLE
JOURNAL

Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawal, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Ooderica, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
Direct Submission
Submitted (17-JUL-2002) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawal, J., Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PEGC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Banh, J., Bowser, L., Chan, M.M., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Ooderica, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Davis, R.W., Theologis, A., and Ecker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

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CDS

BASE COUNT 356 a 289 c 314 g 340 t
ORIGIN
Alignment Scores:
Pred. No.: 1 04e-111 Length: 1299
Score: 1380.50 Matches: 264
Percent Similarity: 75.29% Conservative: 62
Best Local Similarity: 60.97% Mismatches: 92
Query Match: 59.17% Indels: 15
DB: 8 Gaps: 5

US-09-857-612a-14 (1-443) x AY133614 (1-1299)

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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1498)
AUTHORS Haas,B.O., Volkovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
Feidman,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE Full-length messenger RNA sequences greatly improve genome
annotation
JOURNAL Genome Biol. (2002) in press
REFERENCE 2 (bases 1 to 1498)
AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feidman,K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one

percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the Ws or Laer ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
GenSet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.

FEATURES
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BASE COUNT 425 a 322 c 343 g 408 t
ORIGIN

Alignment Scores:

Pred. No.: 1,23e-111 Length: 1498
Score: 1380.50 Matches: 264
Percent Similarity: 75.29% Conservative: 62
Best Local Similarity: 59.97% Mismatches: 92
Query Match: 59.17% Indels: 15
DB: 8 Gaps: 5

US-09-857-612a-14 (1-443) x AY087433 (1-1498)

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RESULT 6
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LOCUS AX037605
DEFINITION Sequence 29 from Patent WO0060095.
ACCESSION AX037605
VERSION AX037605.1 GI:11227019
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi-
s (bases 1 to 1562)
REFERENCE
AUTHORS Banas,A., Stahl,U., Styenne,S., Lemman,M., Ronne,H. and Dahlqvist,A.
TITLE A new class of enzymes in the biosynthetic pathway for the
production of triacylglycerol and recombinant dna molecules
encoding these enzymes

JOURNAL Patent: WO 0060095-A 29 12-OCT-2000;
BASE PLANT SCIENCE GMBH (DE) ; BANAS ANTONI (PL) ; STAHL Ulf (SE) ;
STYENNE STEN (SE) ; LEMMAN MARIT (SE) ; RONNE HANS (SE) ; DAHLQVIST
ANDERS (SE)
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DEFINITION	Oryza sativa chromosome 3 clone OSUNB0011H13, *** SEQUENCING IN		
ACCESSION	AC120983		
VERSION	AC120983.1	GI:20564440	
KEYWORDS	HTG; HTGS; PHASE2.		
SOURCE	Oryza sativa.		
ORGANISM	Oryza sativa		
REFERENCE	Enkaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
AUTHORS	1 (bases 1 to 134188) Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Tallon, L., Gansberger, K., Kim, M., Overton II, L., Bera, J., Tsalirli, T., Krol, M., Jarrahl, B., Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S., Uterbach, T., Feldblyum, T., Yang, Q., Haas, B., Suh, B., Peterson, J., Quackenbush, J., White, O., Salzberg, S., and Fraser, C.		
TITLE	Oryza sativa ssp. japonica cv. Nipponbare OSUNB0011H13 BAC genomic sequence		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 134188)		
AUTHORS	Buell, R.		
JOURNAL	Direct Submission		
COMMENT	Submitted (14-MAY-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submittor. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved. 1 61218: contig of 61218 bp in length * 61219 61256: gap of unknown length * 61257 77652: contig of 16396 bp in length * 77653 77727: gap of unknown length * 77728 131160: contig of 53433 bp in length * 131161 131197: gap of unknown length * 131198 134188: contig of 2991 bp in length. location/Qualifiers 1. 134188 /organism="Oryza sativa" /cultivar="Nipponbare" /db_xref="taxon:4530" /chromosome="3" /clone="OSUNB0011H13" /note="japonica cultivar-group" BASE COUNT 39144 a 28013 c 28230 g 38642 t 159 others ORIGIN		
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DEFINITION	Prunus dulcis lecithin-cholesterol acyl transferase (LCAT1) gene,			PLN 03-JAN-2000
ACCESSION	AF209909			
VERSION	AF209909.1	GI:6653737		
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	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.			
REFERENCE	1 (bases 1 to 833)			
AUTHORS	Ma,R.C. and Oliveira,M.M.			
TITLE	Molecular Cloning of A Lecithin-Cholesterol Acyl Transferase			
JOURNAL	Homolog Gene from Almond (Prunus dulcis)			
REFERENCE	2 (bases 1 to 833)			
AUTHORS	Ma,R.C. and Oliveira,M.M.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-DEC-1999) Lab of Plant Genetic Engineering, Instituto			
	de Biologia Experimental e Tecnologica, Quinta do Marquês,			
	Oeiras/Lisboa, Lisboa Aptd.12-27/80, Portugal			
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REFERENCE
AUTHORS
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FEATURES
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US-09-857-612a-14 (1-443) x AP005640 (1-139534)
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Db 129498 GGGCCGACAAACCTGCTTCTACGTGTCAGACGGAGAGCGTGTGCTCGGCAATGTGG 129557
QY 275 ArgSerSerGluSerAsnLeuTrpLeuLeuProAsnProLysIlePheGlyProGlnLys 294
Db 129558 AGGACCTTCGAGACCGACGATGCCAACCTCCCTCCGCGCGCTGTTGGG---CGCAG 129614
QY 295 ProIleValIleThrProIleArgProTyrSerAlaHisAspMetValAspPheLeuLys 314
Db 129615 CCGATCTGTGTCACCGACGCGAGACTACTTCGCGTACGATATGGAAGATCTCCTTCC 129674
QY 315 AspIleGlyPheProGluGlyValTyrPro----- 324
Db 129675 GCGCTGCGTTTCGTCGAGGGATCGAGCCTTTCAGGTAGGGATGCAACCGGATTTTTT 129734
QY 324 ----- 324
Db 129735 TCCGTTATCCCACTTCTAGTTATTTTTTCTTAAATTTTGTACTACATGTCGGA 129794
QY 325 -----Tyr 325
Db 129795 TAACTACCAACAGGATTTTATATCGGGTAGTGGGACTAACCCACTTGCATCTTATTC 129854
QY 326 GluThrArgIleLeuProLeuIleGlyAsnIleLysAlaProGlnValProIleThrCys 345
Db 129855 AGGACAGCAATGTTGTGAGATGTAACCTCGAGGCGCCATGTGTCGTTGACGTAT 129914
QY 346 IleMetGlyThrGlyValGlyThrLeuGluThrLeuPheTyrGlyLysGlyAspPheAsp 365
Db 129915 ATCATGAGATGGGAGAGAGCGCCAGCGCAATGTGCTACTGGAGCAACTTTCAC 129974
QY 366 GluArgProGluIleSerTyrGlyAspGlyAspGlyThrValAsnLeuValSerLeuLeu 385
Db 129975 AAGGCTCCGGAAGATGATAGTGATGAGATGGGATAGTTAACTGTGTTACATGTTA 130034
QY 386 AlaLeuGlnSerLeuTrpLysGluGluLysAsnGln-----TyrLeuLysValValLys 403

gene	pseudogene"	complement(join(7123..7412,7452..7583,8141..8285,8890..9097,10827..11083))
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gene	complement(join(7123..7412,7452..7583,8141..8285,8890..9097,10827..11083))	/gene="P0614D08.2"
CDS		/note="hypothetical protein"
gene	/codon_start=1	/protein_id="BAB86237.1"
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Db 1214 AGCCGCCAAGAGCAGAGATATCAATGCGAGAGCTGCCCGGAGCGAGACACATTGAGATG 1273
QY 413 LeuLysAspGluValAlaLeu 419
Db 1274 CTAGCCAATGCCACCACTTG 1294

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Search completed: February 15, 2003, 14:56:17
 Job time : 2688 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 15, 2003, 13:14:57 : Search time 215 seconds

(without alignments)
4640.164 Million cell updates/sec

Title: US-09-857-612a-14

Perfect score: 2333
Sequence: 1 MKKEQEGEGLKIEVATLTVV.....GELTINSNHAELSLNFSG 443

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=framer_p2n.model -DEV=xlh
-O=/cgnt2_1/USPTO.spool/US09857612/runtat_11022003_111817_29814/app_query.fasta_1.583
-DB=N.Geneseq_101002 -QPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsunc2 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USBR=US09857612.6CGN_1.1_125.6runtat_11022003_111817_29814 -ICPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV=TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6 -FCGAPEXT=7
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Database :

N_Geneseq_101002: *
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2333	100.0	1332	21	AAA49206 Soybean putative 1
2	2022	86.7	1217	21	AAA49202 Soybean putative 1
3	1380.5	59.2	1299	22	AA501081 Arabidopsis thalia
4	1380.5	59.2	1495	21	AAC47273 Arabidopsis thalia
5	1380.5	59.2	1498	21	AAC39845 Arabidopsis thalia
6	1310	56.2	1562	21	AAC64437 Arabidopsis thalia
7	1310	56.2	1562	21	AAC64447 Arabidopsis thalia
8	913.5	39.2	1500	21	AAA49204 Corn putative leci
9	739.5	31.7	1660	21	AAA49205 Corn putative leci
10	717	30.7	1440	21	AAA49203 Corn putative leci
11	612	26.2	1236	19	AAV68568 Murine kidney leci
12	610	26.1	1236	19	AAV68566 Human heart leci
13	610	26.1	2680	20	AA234023 Human PRO540 nucle
14	610	26.1	2680	20	AAC78492 Human PRO540 (UNO3
15	610	26.1	2680	21	AAA88516 Human PRO540 CDNA
16	610	26.1	2680	22	AAC91566 Human PRO540 CDNA
17	610	26.1	2680	24	ABK69967 CDNA encoding huma
18	610	26.1	2681	22	AAH14618 Human cDNA sequenc
19	610	26.1	2720	22	AAK94279 Human full-length
20	608	26.1	1137	19	AAV68561 Human heart leci
21	608	26.1	1146	19	AAV68564 Human heart leci
22	606	26.0	1137	19	AAV68563 Murine leci
23	597	25.6	2687	21	AAA26392 Human secreted pro
24	596	25.5	1332	19	AAV68567 Human kidney leci
25	594	25.5	1233	19	AAV68562 Human kidney leci
26	594	25.5	1242	19	AAV68565 Human kidney leci
27	560	24.0	1824	23	ABL21223 Drosophila melanog
28	554	23.7	1135	22	AA501095 Corn sterol acyltr
29	543	23.3	1358	8	AAAT0191 DNA clone p12 enc
30	541	23.2	1323	24	ABK87900 CDNA encoding huma
31	541	23.2	1744	20	AA232180 Human leci
32	541	23.2	1744	22	AA202648 Human leci
33	541	23.2	1744	24	ABN95747 Gene #2245 used to
34	541	23.2	1744	24	ABK35510 Human endometrial
35	541	23.2	4308	22	AAAD02649 Human endometrial
36	493	21.1	563	21	AAA69662 Drosophila melanog
37	490.5	21.0	4024	23	ABL21222 Plnus radiata leci
38	458.5	19.7	921	21	AAA49202 Corn putative leci
39	428	18.3	264	22	AA501087 Soybean sterol acy
40	376	16.1	353	21	AAA69561 Plnus radiata leci
41	372.5	16.0	542	21	AAA49200 Corn putative leci
42	344	14.7	273	22	AA501088 Soybean sterol acy
43	281.5	12.1	5700	24	ABK87899 Human leci
44	281.5	12.1	6901	18	AA78853 Human leci
45	248	10.6	778	22	AAH06918 Human cDNA clone (

ALIGNMENTS

RESULT 1
ID AAA49206 standard: CDNA: 1332 BP.

AC AAA49206;

DT 12-DEC-2000 (first entry)

DE Soybean putative leci

DE Soybean putative leci

DE Soybean putative leci

DE Soybean putative leci

DE Soybean putative leci

DE Soybean putative leci

DE Soybean putative leci

DE Soybean putative leci

FT /product= "lecithin:cholesterol acyltransferase"
EC_number= "2.3.1.43"
XX WO200032791-A2.
XX
XX
PD 08-JUN-2000.
XX
XX 02-DEC-1999: 99WO-US28586.
XX
XX 03-DEC-1998: 98US-0110782.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
XX Cahoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;
DR WPI: 2000-412337/35.
XX P-PSDB: AAB01211.
XX
XX Polynucleotide encoding plant lecithin:cholesterol acyltransferase
PT enzyme useful for producing transgenic plants and for producing
PT antibodies specific to which is useful for screening cDNA expression
PT libraries -
XX
XX
PS Claim 2: page 46; 49pp; English.
XX
XX The present sequence is a putative coding sequence for a soybean
CC lecithin:cholesterol acyltransferase (also known as
CC phosphatidylcholine-sterol O-acyltransferase). This enzyme is found
CC associated with high-density lipoproteins and Apolipoprotein-AI and -D.
CC The gene and protein can be used to produce transgenic plants which have
CC increased lipid metabolism and membrane fluidity, and therefore increased
CC resistance to heat and/or cold shock, to alter the content of phytosterol
CC or lecithin in grains and to identify potential herbicides.
XX
XX
SQ Sequence 1332 BP; 385 A; 282 C; 289 G; 376 T; 0 other:

Alignment Scores:
Pred. No.: 1,03e-240 Length: 1332
Score: 2333.00 Matches: 443
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-857-612a-14 (1-443) x AAA49206 (1-1332)
OY 1 MetLysLysGluGluGluGluLeuLysIleGluValAlaThrLeuThrValThrVal 20
DB 1 ATGAG 60
OY 21 ValValValMetLeuSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 61 GTTGTGTGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 120
OY 41 LeuLeuProGlyAsnGlyLysGluGluGluGluGluGluGluGluGluGluGluGlu 60
DB 121 CTAATAACCGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
OY 61 SerThrPheIleCysGluSerTrpTrpProLeuIleLysLysLysAsnGlyTrpPhe 80
DB 181 TCTACTTTCATGTCGGAATCATGTAACCTCTCATCAAGAAAGATGATGATGATGAT 240
OY 81 LeuTrpPheAspSerSerValIleLeuAlaProPheThrGlnCysPheAlaGluArg 100
DB 241 CTTTGTTTGATTCAGATGCTCATCTGCTCTTCACATCATGCTTTCGCGAAGCAG 300
OY 101 ThrLeuHisTyrHisGlnGluLeuAspAspTyrPheAsnThrProGlyValGluThrArg 120
DB 301 ACCCTTCATTTACACCAAGAACTCGATGATCTTCAACACCTCGGGGTTGAGACCCG 360
OY 121 ValProHisPheGlySerThrAsnSerLeuLeuTyrLeuAsnProArgLeuHisHisIle 140
DB 361 GTCCCTCACTTGGTTCACCAACTCTTCTCTATCTCAATCTCCTCAAGCATATTC 420

OY 141 ThrGlyTyrMetAlaProLeuValAspSerLeuGlnLysLeuGlyTyrAlaAspGlyGlu 160
DB 421 ACCGATATACATGACACCCCTGATGATTCATTCACAAAGCCTTGATACGCTGATGATG 480
OY 161 ThrLeuPheGlyAlaProTyrAspPheArgTyrGlyLeuAlaIleGluGlnHisProSer 180
DB 481 ACTCTGTTTGGACCCCTTATGACTTATGATATGCTGATGCTGATGCTGATGCTGAT 540
OY 181 GluValGlySerLysPheLeuLysAspLeuLysAsnLeuIleGluGlnAlaSerAsnSer 200
DB 541 CAAGTGGGTTCCAAAGTTCCTCCAAAGATCTTAAGAAATTTGATAGAACAGCAAGCAATTC 600
OY 201 AsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyLysLeuPheValLeuGln 220
DB 601 AATAATGGAGAGCCAGTGAATCTTCTCCACAGATTAGAGAGCCTTATTTGCTCAACA 660
OY 221 LeuLeuAsnArgAsnProProSerTrpArgLysLysPheIleLysHisPheIleAlaLeu 240
DB 661 CTACTAATAATAGAAACCCCTCTTGGCCCAAAAAATTCATCAAAACCTTCATTCCTCTT 720
OY 241 SerAlaProTrpGlyLysAlaIleAspGluMetTyrThrPheAlaSerGlyAsnThrLeu 260
DB 721 TCAGCTCCATGGGGTGGTGTCTATAGACGAATGTACACCTTTCATCTGGCAACACTTTC 780
OY 261 GlyValProLeuValAspProLeuLeuValArgAspGluGlnArgSerSerGluSerAsn 280
DB 781 GGAGTCCCTCCTAGTAGACCTTATATAGAGAGGATGAAACAAAGAGCTCCGAGACTAAC 840
OY 281 LeuTrpLeuLeuProAsnProLysIlePheGlyProGlnLysProIleValIleThrPro 300
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OY 301 IleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIleGlyPheProGlu 320
DB 901 ATTAGCCTTATTCACGCTCATGACATGCTGATTTTCTAAAGACATTTGTTTCTGTA 960
OY 321 GlyValTyrProTyrGluThrArgIleLeuProLeuIleGlyAsnIleLysAlaProGln 340
DB 961 GGGGTTTATCCTTATATGAACACGAATTTACCTTGATAGGAGAACATAAAGACACACAA 1020
OY 341 ValProIleThrCysIleMetGlyThrGlyValGlyTyrLeuGluThrLeuPheTyrGly 360
DB 1021 GTGCCATTAACCTTGTATTTATGGAGAGGAGTGGGAACCTTGGAAACATTTGTTATGG 1080
OY 361 LysGlyAspPheAspGluArgProGluIleSerTyrGlyAspGlyAspGlyThrValAsn 380
DB 1081 AAAGTGATTTTGCATGAACGCCAGAAATATCATATGGGATGCTGATGGAACGGTGAAAC 1140
OY 381 LeuValSerLeuLeuAlaLeuGlnSerLeuTrpLysGluGluLysAsnGlnTyrLeuLys 400
DB 1141 TTGGTAGCTGTGGCGCTTCATCATCATATGGAAGAGAGAGAAATCAATACCTTAA 1200
OY 401 ValValLysIleAspGlyValSerHisThrSerIleLeuLysAspGluValAlaLeuAsn 420
DB 1201 GTGGTTAAAGATGATGGGGTGTCTCATCTTCAATTAAGGATGAATTTCCACATAAT 1260
OY 421 GluIleValGlyGluIleThrSerIleAsnSerHisAlaGluLeuGlyLeuSerAsnLeu 440
DB 1261 GAAATATGATGGTGAATTTCTTCAATTAATTTCTCATGCTGAGCTGCGTTTAAGTAATTTG 1320
OY 441 PheSerGly 443
DB 1321 TTTTGGGG 1329

RESULT 2
AAA49202
ID AAA49202 standard; cDNA; 1217 BP.
XX
XX AAA49202;
AC
XX
XX
DT 12-DEC-2000 (first entry)
XX

DE	Soybean putative lecithin:cholesterol acyltransferase gene #1.			
XX				
KW	Soybean: lecithin:cholesterol acyltransferase: phytosterol:			
KW	phosphatidylcholine-sterol O-acyltransferase; heat shock; cold shock; ss.			
XX				
OS	Glycine max.			
XX				
EH	Key	Location/Qualifiers		
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FT		/partial		
FT		/Ec_number= "2.3.1.43"		
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PN	WO200032791-A2.			
PD	08-JUN-2000.			
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PF	02-DEC-1999;	99WO-US28586.		
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PR	03-DEC-1998;	98US-0110782.		
XX				
PA	(DUPO) DU PONT DE NEMOURS & CO E I.			
XX				
PI	Canoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ,			
DR	WPI: 2000-412337/35.			
DR	P-PSDB: AAB01207.			
XX				
PT	Poly nucleotide encoding plant lecithin:cholesterol acyltransferase			
PT	enzyme useful for producing transgenic plants and for producing			
PT	antibodies specific to which is useful for screening cDNA expression			
PT	libraries			
XX				
PS	Claim 2, Page 38; 49pp; English.			
XX				
CC	The present sequence is a putative coding sequence for a soybean			
CC	lecithin:cholesterol acyltransferase (also known as			
CC	phosphatidylcholine-sterol O-acyltransferase). This enzyme is found			
CC	associated with high-density lipoproteins and Apolipoprotein-A1 and -D.			
CC	The gene and protein can be used to produce transgenic plants which have			
CC	increased lipid metabolism and membrane fluidity, and therefore increased			
CC	resistance to heat and/or cold shock, to alter the content of phytosterol			
CC	or lecithin in grains and to identify potential herbicides.			
XX				
SQ	Sequence 1217 BP; 346 A; 250 C; 262 G; 359 T; 0 other;			
Alignment Scores:				
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	Score:	2022.00	Matches:	381
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	Best Local Similarity:	100.00%	Mismatches:	0
	Query Match:	86.67%	Indels:	0
	DB:	21	Gaps:	0
US-09-857-612A-14 (1-443) x AAA49202 (1-1217)				
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DB	3	TTTCATCTGGGAATCATGATGACCTCTTCATCCAAAGAAAAGATGGATGGTTCAGACTTTGG	62	
QY	83	PheAspSerSerValIleLeuAlaPProPheThrGlnCysPheAlaGluArgMetThrLeu	102	
DB	63	TTTGGATTCACAGTGTCTACTTGTCTCTTTTCACATCAATGCTTTGGCCGAACCATGACCTT	122	
QY	103	HisTrpHisGlnGluLeuAspAspTrpPheAsnThrProGlyValGluTrpArgValPro	122	
DB	123	CATTACACCAAGAACTCATGATTCATCTCAACACATCCTGGGGTGGAGACCGGCTCCT	182	
QY	123	HisPheGlySerThrAsnSerLeuLeuPyrLeuAsnProArgLeuLysHisIleThrGly	142	
DB	183	CACTTTGGTTCACCAACTCTCTTCTCTATCTCAAACTCTGCTCAAGCATATCACCGGA	242	

QY	143	TYR	MetAlaProLeuValAspSerLeuGlnIysLeuGlyTyrAlaAspGlyGluThrLeu	162
Db	243	TACATGGACACCCCGCTAGATCATACAAACCTGGCTACGATGTAGACTCTG	302	
QY	163	PheGlyAlaProTyrAspPheArgTyrGlyLeuAlaIaGluGlyPHisProSerGlnVal	182	
Db	303	TTTGGAGCCCTTATGACTTTAGATTAGTCTAGCTGTAAGGATCACCTTCACAAATG	362	
QY	183	GlySerIysPheLeuIysAspLeuIysAsnLeuIleGluGluAlaSerAsnSerAsnAsn	202	
Db	363	GGTTTCCAAAGTTCCTCAAAAGATCTTAAGAAATTTGATAGAAAGAACAAACAAATTC	422	
QY	203	GlyIysProValIleLeuLeuSerHisSerLeuGlyGlyLeuPheValLeuGlnLeu	222	
Db	423	GGGAAGCCAGATACCTTCTCTCCACAGTTTGGAGGCGCTATTGTCTTACAACTACTA	482	
QY	223	AsnArgAsnProProSerTyrArgIysIysPheIleIysHisPheIleIleuSerAla	242	
Db	483	AATAGAAACCCCCCTTGTGGCGCAAAAAATTCATAAACCTCAATGTCTCTTTCACCT	542	
QY	243	ProTyrGlyGlyAlaIleAspGluMetTyrThrPheAlaSerGlyAsnThrLeuGlyVal	262	
Db	543	CCATGGGGTGGTGGTATAGACGAATGTATACCTTTCGATCTGGACACCTTGGGATG	602	
QY	263	ProLeuValAspProLeuLeuValArgAspGluGlnArgSerSerGlnSerAsnLeuTrp	282	
Db	603	CCCCTAGAGCACCTTATTATAGTAGAGGATGAACAAGAACCTCGACAGTAACTCTTGG	662	
QY	283	LeuLeuProAsnProIysIlePheGlyProGlnIysProIleValIleThrProIleArg	302	
Db	663	CTTTTGGCTTAACCCCAAAATTTTGGTCCCAAAAAACCAATGTGTATTAATCTCAATTAGG	722	
QY	303	ProTyrSerAlaHisAspMetValAspPheLeuIysAspIleGlyPheProGluGlyVal	322	
Db	723	CCTTATTCAGCTCATGACATGATGTTGATTTCTTAAAGACATTGGTTTCTCAAGCGTT	782	
QY	323	TyrProTyrGluThrArgIleLeuProLeuIleGlyAsnIleIysAlaProGlnValPro	342	
Db	783	TATCCTTATGAACACACAATTTTACCTTGATAGGGAACATGTAAAGCACACAAAGTCCCT	842	
QY	343	IleThrCysIleMetGlyThrGlyValGlyThrLeuGlnThrLeuPheTyrGlyGlyGly	362	
Db	843	ATACTGTATATTATGGGAACGGGAGTGGGAACCTTGGAACAATGTATTATGGGAAAGT	902	
QY	363	AspPheAspGluArgProGluIleSerTyrGlyAspGlyAspGlyThrValAsnLeuVal	382	
Db	903	GATTTTGATGACCGCCAGAAATATCATATAGGGGATGTGATGGAACGGTGAACCTTGGTG	962	
QY	383	SerLeuLeuAlaLeuGlnSerLeuTrpIysGluGluIysAsnGlnThrLeuIysValVal	402	
Db	963	AGCTGTATGGCGCTTCAATCATCATATGGAAAGAGAGAAAAATCATATACCTTAAATGGTT	1022	
QY	403	LysIleAspGlyValSerHisThrSerIleLeuIysAspGluValAlaLeuAsnGluIle	422	
Db	1023	AAGATAGATGGGGTCTCATCTACTCATCTTAAGAGATGAAGTGGACATTAATTAATA	1082	
QY	423	ValGlyGluIleThrSerIleAsnSerHisAlaGluLeuGlyLeuSerTrsLeuPheSer	442	
Db	1083	GTAAGTGAGATTACTTAATTAATTCATGCTGACAGCTGGTTTATAGTAATTTGTTTTCG	1142	
QY	443	Gly 443		
Db	1143	GGG 1145		
RESULT 3				
AAS01081				
ID AAS01081 standard; DNA: 1299 BP.				
NC AAS01081;				
XX 31-MAY-2001 (first entry)				
DT				
XX Arabidopsis thaliana sterol acyltransferase LCAT1 DNA.				

PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148365.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
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PR 29-SEP-1999; 99US-0156596.
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PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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PR 13-OCT-1999; 99US-0158293.
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PR 18-OCT-1999; 99US-0159584.
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 23-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:

Pred. No.: 3.07e-138
Score: 1380.50
Percent Similarity: 75.29%
Best Local Similarity: 60.97%
Query Match: 59.17%
DB: 21

Length: 1495
Matches: 264
Conservative: 62
Mismatches: 92
Indels: 15
Gaps: 5

US-09-857-612A-14 (1-443) x AAC47273 (1-1495)

QY 1 MetLysLysGluGlnGluGluGluLysIleGluValAlaThrLeuThrValThrVal 20
DB 82 ATGAAAAA-----ATATCTCATATTATTCGTAGCTACGATAC 126

QY 21 ValValValMetLeuSerLeuLeuGluGluGluGluGluGluGluGluGluGlu 40
DB 127 GTTGTGTGACGATGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 186

QY 41 LeuIleProGluYAsnGluYAsnGluGluGluGluGluGluGluGluGluGluGlu 60
DB 187 CTGGTTCCAGAAACGAGAGTACCGATGAGATGAGATGAGATGAGATGAGATGAG 246

QY 61 SerThrPheIleGluGluSerThrPheIleGluGluGluGluGluGluGluGlu 79
DB 247 AGTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306

QY 80 ArgLeuTrpPheAspSerSerValIleLeuAlaProPheThrGlnCysPheAlaGlu 99
DB 307 AGGCTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 366

QY 100 MetThrLeuHisThrHisGlnGluLeuAspAspTrpPheAsnThrProGluValGluThr 119
DB 367 ATGATGTTGTACTATGACCCCTGATTTGATTTACCAAAATGCTCTGCTGCTCAAC 426

QY 120 ArgValProHisPheGluSerThrAsnSerLeuLeuLeuLeuLeuLeuLeuLeu 139
DB 427 CGGTTCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486

QY 140 IleThrGluThrMetAlaProLeuValAspSerLeuGln--LysLeuGluThrAlaAsp 158
DB 487 GCACATCTTACATGGAACATTTGTTGGAAGCTGAGAAATAAATGCGGATGTTAAC 546

QY 159 GluGluThrLeuPheGluValProTrpAspPheAspGlyGlyLeuAlaIleGluGluHis 178
DB 547 GACCAAAACCATCTGAGACCTCATATGATTTGAGGTAGGCTGCTGCTGCTGCTGCTGCT 606

QY 179 ProSerGluValGluSerLysPheLeuLysAspLeuLysAsnLeuLeuGluGluAlaSer 198
DB 607 CCGTCCCGTGTACCTCAGACATTTCCACAGACCTCAACATTTGGTGAATAAACTAC 666

QY 199 AsnSerAsnAsnGluLysProValIleLeuLeuSerHisSerLeuGluGlyLeuPheVal 218
DB 667 ACGAGAAACGAGAAAGCAGATGATCTCTCCATAGGCTGAGAGACTTTTTCGC 726

QY 219 LeuGlnLeuLeuAsnArgAsnProProSerTrpArgGlyLysPheIleLysHisPheIle 238
DB 727 CTTCATTTCTCAACCGTACACACCCCTTCATGCGCCGCAAGTACATCAACACTTTGTT 786

QY 239 AlaLeuSerAlaProTrpGluGluAlaIleAspGluMetTrpThrPheAlaSerGluAsn 258
DB 787 GCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846

QY 259 ThrLeuGluValProLeuValAspProLeuLeuValArgAspGluGlnArgSerSerGlu 278
DB 847 ACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906

QY 279 SerAsnLeuTrpLeuLeuProAsnProLysIlePheGluProGln---LysProIleVal 297
DB 907 ACTAACCAATGCTACTTCCATCCAAAGTGTTCACGACAGAACTTAACCGCTTGC 966

QY 298 IleThrProIleArgProTrpSerIleHisAspMetValAspPheLeuLysAsnIleGly 317
DB 967 GTAACCTCCAGCTTAACCTACAGCTTACAGATGATGATGATGATGATGATGATGATG 1026

QY 318 PheProGluGluValTyrProTrpGluThrArgIleLeuProLeuIleGluAsnIleLys 337
DB 1027 TTCTCACAAGAGGTGTGTGCTTACAAAGACAGAGTGTTCCTTAACAGAGAGAGCTAATG 1086

QY 338 AlaProGluValProIleThrCysIleMetGlyThrGluValGlyThrLeuGluThrLeu 357

Db 1087 ACTCCGGAGTCCAGTCACTTCATATATGCGAGAGAGATTGATACACCGAGGCTTTG 1146
Qy 358 Phetyrclgylgysgllyaspheaspluarprocluliesertyrlyaspgllyaspclly 377
Db 1147 ATGTATGGAAGAGAGATTTCGATACACACAGATTAACTATGCGATGCGACATCGG 1206
Qy 378 ThrValnsleuValSerleuLeuAlaLeuGlnSerleuTrpLysglulLysasnGln 397
Db 1207 ACGGTATATTGGCGAGCTTACAGACTTTG-----AAAGTCGAT 1245
Qy 398 TyrleuLysValValLysIleAspGlyValSerHisThrSerIleLeuLysAspGluVal 417
Db 1246 AGCTTGACACACCGTGAATGATGAGTTTCGATCATCTATATCTTAAAGACGAGATC 1305
Qy 418 AlaLeuAsnGluIleValAlaGlyLulIleThrSerIleasn 430
Db 1306 GCACCTTAAAGGATTATGACGACATTTCAATTATTAAAT 1344
RESULT 5
AAC39845
ID AAC39845 standard; DNA; 1498 BP.
XX
AC AAC39845;
XX
DT 17-OCt-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 26113.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0129845.
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PR 30-APR-1999; 99US-0132407.
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PR 06-MAY-1999; 99US-0132486.
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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
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PR 21-MAY-1999; 99US-0135353.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 18-JUN-1999; 99US-0139461.
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PR 21-JUN-1999; 99US-0139817.
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PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
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PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
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PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.

DB 967 GTACTCCAGTAACTACAGATGATCGTTTTCAGACATTGCA 1026
QY 318 PhetroluglyValIYrProTgIuThraGleleuProleuIleGlyAsnIleYs 337
DB 1027 TTCCTCAAGAGTGTGCTTACAGCAAGAGTGTTCCTTACAGAGAGGACTGATG 1086
QY 338 AlapProGlnValIProIleThrCysIleMetGlyThrGlyValIglYhrLeuGluThrLeu 357
DB 1087 ACTCCGGAGTGCAGTCACTTCATATATGAGAGAGTGTGATACCCGAGCTTTTG 1146
QY 358 PhetTyrGlyGlyAspPheAspGluArProGluIleSerTyrGlyAspGlyAspGly 377
DB 1147 ATGATGAGAAAGAGATTCGATACAGCAACGAGATTAGTATGAGATGAGATCGG 1206
QY 378 ThrValAsnLeuValSerLeuLeuAlaLeuGlnSerLeuTyrPlyGluGluIlyAsnGln 397
DB 1207 ACGGTTAATTTGGCGACTTACGAGCTTTG-----AAAGTCGAT 1245
QY 398 TyrLeuLysValValIlySleAspGlyValSerHisThrSerIleLeuLysAspGluVal 417
DB 1246 AGCTTGAAACACCGTAGAGATGATGCACTTCGATACATCTATATCTTAAAGACAGATC 1305
QY 418 AlaLeuAsnGluIleValIglYgluIleThrSerIleAsn 430
DB 1306 GCACCTAAAGAGATTATGAGACAGATTTCATATTAT 1344
RESULT 6
ID AAC64437 standard; DNA: 1562 BP.
XX AAC64437;
XX 12-FEB-2001 (first entry)
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:10.
XX PDAT: phospholipid:diacylglycerol acyltransferase: triacylglycerol;
KM TAG; EST: expressed sequence tag; fatty acid; oil content; ds.
OS Arabidopsis thaliana.
XX
XX WO200060095-A2.
XX
XX 12-OCT-2000.
XX
XX 28-MAR-2000: 2000WO-EP02701.
XX
XX 01-APR-1999: 99EP-0106656.
XX 10-JUN-1999: 99EP-0111321.
XX 07-FEB-2000: 2000US-0180687.
XX
XX (BADT) BASF PLANT SCI GMBH.
XX
XX Dahlglyst A, Stahl U, Lenman M, Banas A, Ronne H, Styhme S;
XX WPI, 2000-665012/64.
XX
XX
XX Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT pathway for triacylglycerol production and DNAs encoding them, useful
PT for producing triacylglycerol, or for transforming any cell or organism
PT to increase oil content -
XX
PS Claim 6: Page 59; 97pp: English.
XX
XX The present invention describes an enzyme for catalysing (in an
CC acyl-CoA-independent reaction) the transfer of fatty acids from
CC phospholipids to diacylglycerol in the biosynthetic pathway for the
CC production of triacylglycerol (TAG). The enzyme is designated as
CC phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and
CC the nucleotides encoding them are useful for producing TAG and/or
CC TAG with uncommon fatty acids. The enzyme and the nucleotide are
CC also useful for transforming any cell or organism in order to be

CC expressed in this cell or organism and result in an altered, preferably
CC increased oil content of this cell or organism. The present sequence
XX represents the Arabidopsis thaliana PDAT genomic DNA.
SQ Sequence 1562 BP: 441 A; 312 C; 367 G; 442 T; 0 other;
Alignment Scores:
Pred. No.: 1,24e-130 Length: 1562
Score: 1310.00 Matches: 264
Percent Similarity: 62.57% Conservative: 62
Best Local Similarity: 50.67% Mismatches: 92
Query Match: 56.15% Gaps: 104
DB: 21
US-09-857-612a-14 (1-443) x AAC64437 (1-1562)
QY 1 MetLysLysGluGluGluGluGlyLeuLysIleGluValAlaThrLeuThValThrVal 20
DB 1 ATGAAAAA-----ATATCTCACATATATTCGATGATGCGATATCTC 45
QY 21 ValValValMetLeuSerLeuLeuCysThrCysGlyAlaSerAsnLeuAspProLeuIle 40
DB 46 GTTGGTGACGAGTACCTCGATGTGTACAGCTGTGGGTACCAACGTGTACCTTTGATT 105
QY 41 LeuIleProGlyAsnGlyGlyAsnGlnLeuGluAlaArGluThrAsnGlnTyrLysPro 60
DB 106 CTGTTCCAGAAACGAGAGGTATACAGCTAGAGTACGCTGGACAGAGATACAGCA 165
QY 61 SerThrPheIleCysGluSerTrp--TyrProLeuIleLysLysLysAsnGlyTyrPhe 79
DB 166 AGTAGTGTCTGTGTGACGACGCTGTTATATCCATTAAGAGAGTGGTATGCTTT 225
QY 80 ArgLeuTrpPheAspSerSerValIleLeuAlaProPheThrGlnCysPheAlaGluArg 99
DB 226 AGGCTATGTTGATGACGACGAGTGTATGTCTCCCTTCACAGAGGCTTACAGCATGCA 285
QY 100 MetThrLeuHisTyrHisGlnGluLeuAspAspTyrPheAsnThrProGlyValGluThr 119
DB 286 ATGATGTTGTACTATGACCCGATTTGGATGATTACCAAAATGCGTCGTCCAAAC 345
QY 120 ArGValProHisPheGlySerThrAsnSerLeuLeuTyrLeuAsnProArgLeuLysHis 139
DB 346 CGGTTCTCATTTCTGTCGACCAACATCACTTATACCTGACCCGTCGCGTT- 404
QY 139 ----- 139
DB 405 AGTACTTCCAAAGATATATCATTTTGGGACATTTGCATATAGCAAAATAGACATAAAT 464
QY 139 ----- 139
DB 465 TTGGGGATTATGTTATATCATATATCATTTATGCTAGTGGTAAATGTGAGTGTAT 524
QY 139 ----- 139
DB 525 GTTACTATAGTTAATGTGAGTGTATGTGATTTTCCATTAAATGAAGTAAAGATTG 584
QY 139 ----- 139
DB 585 TCGTTTAATATGTTGCTATGTCATGAGATTAAGAGCACTATGTAATGTACCTTAA 644
QY 140 ----- 151
DB 645 TAATAAGTTTGATTTGCAGAGATCCCATCTTACATGGAACATTTGTGTAACCTCTA 704
QY 152 Gln---LysLeuGlyTyrAlaAspGlyGluThrLeuPheGlyAlaProTyrAspPheArg 170
DB 705 GAGAAATAATCGGGTATGTTAAGCAACCAACATCTAGAGAGCTCATATGATTTACAG 764
QY 171 TyrGlyLeuAlaIleGluGlyHisProSerGlnValIglYserLysPheLeuLysAspLeu 190
DB 765 TACGGCTGTGGCTGTGGGACCCGTCGCTGAGGCTCAACATCTTACAGACCTC 824
QY 191 LysAsnLeuIleGluGluAlaSerAsnSerAsnGlyLysProValIleLeuLeuSer 210

Db 465 TTGGGGATATATGTATATCATATATCCATTTATATGCTAGTCGTAATGAGTGTAT 524
 QY 139 ----- 139
 Db 525 GTTAGTATAGTAAATGTGAGTGTATATGATTTCCATTTAAATGAAGTAGAAAGTTG 584
 QY 139 ----- 139
 Db 585 TCGTTATATATGTTGCTATGATCATGAAATTATAGACACATATGTAATAGTACTTAA 644
 QY 140 ----- 140
 Db 645 TAATAGGTTGATTTGACAGATGCCACATCTTACATGAAACATTTGTGTAAGACCTCTA 704
 QY 152 Gln---lysleuGlyTyrAlaAspGlyLutThrLeuPheGlyAlaProTyrAspPheArg 170
 Db 705 GAGAAAAATCGGGTATGTTAACGACCAACCATCTAGAGCTCCATGATTTTCAGG 764
 QY 171 TyrGlyLeuAlaAlaGlyLysHisProSerGlnValGlySerLysPheLeuLysAspLeu 190
 Db 765 TACGGCTCGGCTGCTCGGGCCACCGCCGCTGTAGCTTACACACTTCTTACAAAGACCTC 824
 QY 191 LysAsnLeuIleGlyLysAlaSerAsnSerAsnAsnGlyLysProValIleLeuLeuSer 210
 Db 825 AAACAATGTGTGAAAAAACTAGACGAGAGAGAAAGCAAGCCAGTATCTCTCC 884
 QY 211 HisSerLeuGlyGlyLeuPheValLeuGlnLeuLeuAsnAlaGlnProProSerTyrArg 230
 Db 885 CATAGCCCTAGAGAGATTTGCTCTCCATTTCTCAACCGCTACACCCTTCACAGGCGC 944
 QY 231 LysLysPheIleLysHisPheIleAlaLeuSerAlaProTyrGlyAlaIleAspGlu 250
 Db 945 CGCAAGTACATCAAAACACTTTGTGCACCTCGCTGCGCATGGGGTGGAGACATCTCTAG 1004
 QY 251 MetTyrThrPheAlaSerGlyAsnThrLeuGlyValProLeuValAspProLeuLeuVal 270
 Db 1005 ATGAAGACATTTGCTTGGCAACACACTCGGTGCCCTTAGTTAACCCTTTGGTGTCTC 1064
 QY 271 ArgAspGluGlnArgSerSerGlnSerAsnLeuThrLeuProAsnProLysIlePhe 290
 Db 1065 AGAGCGCATCGAGAGACCTCCGAGATACCAATGGCTACTTCCATTCACCAAACTGTCTT 1124
 QY 291 GlyProGln---LysProIleValIleThrProIleArgProTyrSerAlaHisAspMet 309
 Db 1125 CACGACAGAACTAAACCCCTTGTGTAACCTCCACAGTTACTACACAGCTTACGAGATG 1184
 QY 310 ValAspPheLeuLysAspIleGlyPheProGluGlyValTyrProTyrGlyThrArgIle 329
 Db 1185 GATGGGTTTTTGGACAGATGTGATTCACAGAGAGTTGGCTTACAGCAAGACTG 1244
 QY 330 LeuProLeuIleGlyAsnIleLysAlaProGlnValProIleThrCysIleMetGlyThr 349
 Db 1245 TTGGCTTTAACGAGAGACTGATGCTCCGGAGTCCAGTCTTGCATATATGGGAGA 1304
 QY 350 GlyValGlyThrLeuGluThrLeuPheTyrGlyLysGlyAspPheAspGluArgProGlu 369
 Db 1305 GGAGTGTATACACCGAGGAGTTTGTATGTAAGAAAAGAGATTCGATACCAACAGAGAG 1364
 QY 370 IleSerTyrGlyAspGlyAspGlyThrValAsnLeuValSerLeuLeuAlaLeuGlnSer 389
 Db 1365 ATTAGATATGAGATGAGAGTGGAGCGTTAATTTGGCGACTTACAGACTTGG----- 1418
 QY 390 LeuTyrLysGluGluLysAsnGlnTyrLeuLysValValLysIleAspGlyValSerHis 409
 Db 1419 ----- 1419
 QY 410 ThrSerIleLeuLysAsnGluValAlaLeuAsnGlnIleValGlyGlnIleThrSerIle 429
 Db 1464 ACATCTATACTTAAAGACGAGATGCACTTAAAGAGATTATGAAACAGATTTCATTTATTT 1523
 QY 430 Asn 430
 |||

Db 1524 AAT 1526
 RESULT 8
 ID AAA49204
 AAA49204 standard; cDNA; 1500 BP.
 AC AAA49204;
 XX
 DT 12-DEC-2000 (first entry)
 DE Corn putative lecithin:cholesterol acyltransferase gene #4.
 KW Corn; lecithin:cholesterol acyltransferase; phytosterol;
 XX phosphatidylcholine-sterol O-acyltransferase; heat shock; cold shock; ss.
 OS Zea mays.
 XX
 FH Key Location/Qualifiers
 FT CDS 24..1277
 FT /*tag= a
 FT /product= "lecithin:cholesterol acyltransferase"
 FT /EC_number= "2.3.1.43"
 XX
 PN WO200032791-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28586.
 XX
 PR 03-DEC-1998; 98US-0110782.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Cahoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;
 DR WPI; 2000-412337/35.
 XX P-PSDB; AAB01209.
 PT Polynucleotide encoding plant lecithin:cholesterol acyltransferase
 PT enzyme useful for producing transgenic plants and for producing
 PT antibodies specific to which is useful for screening cDNA expression
 PT libraries -
 XX
 PS Claim 2; Page 41-42; 49pp; English.
 XX
 CC The present sequence is a putative coding sequence for a corn
 CC lecithin:cholesterol acyltransferase (also known as
 CC phosphatidylcholine-sterol O-acyltransferase). This enzyme is found
 CC associated with high-density lipoproteins and Apolipoprotein-AI and -D.
 CC The gene and protein can be used to produce transgenic plants which have
 CC increased lipid metabolism and membrane fluidity, and therefore increased
 CC resistance to heat and/or cold shock, to alter the content of phytosterol
 CC or lecithin in grains and to identify potential herbicides.
 CC
 SQ Sequence 1500 BP; 304 A; 469 C; 454 G; 271 T; 2 other:
 Alignment Scores:
 Pred. No.: 4,97e-88 Length: 1500
 Score: 913.50 Matches: 180
 Percent Similarity: 60.29% Conservative: 69
 Best Local Similarity: 43.58% Mismatches: 155
 Query Match: 39.16% Indels: 9
 Db: 21 Gaps: 4
 US-09-857-612a-14 (1-443) x AAA49204 (1-1500)
 QY 19 ThrValValValValMetLeuSerLeuLeuSerTyrCysGlyAlaSerAsnLeuAspPro 38
 Db 60 ACGATCGTGTGTCCTCAAAATTTGCGAGCACGACGAGCGCCGACCGAAGACAGCTGCCGCC 119
 QY 39 LeuIleLeuIleProGlyAsnGlyLysGlnLeuGluAlaArgLeuThrAsnGlnTyr 58
 Db 120 GTGTTGTGTGTGCGCGGGTACGCCCAACAGAGCTCGAGCGGGCGCTCACGAGAGCTGTAC 179

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Oy 59 LysProSerThrPheIleCysGluSerTrpTyProLeuIleLysLysAsnGlyTrp 78
    |||||::: |||
Db 180 CACCGCTCGTCAACGGCGGCG-----CGGCACAAGGGAAAGGCTGG 221
Oy 79 PheArgLeuTrpPheAspSerSerValIleLeu---AlaProPheThrGlnCysPheAla 97
    |||||::: |||
Db 222 TTCGGCTTACTTCACTACACAGCGCGGTGAGAGCGCGCCGACCTGGCTGTTCGGCC 281
Oy 98 GluArgMetThrLeuIleuIleuTrpHisGlnGluLeuAspAspTrpPheAsnThrProGlyVal 117
    |||::: |||
Db 282 GACGACATGCCCGCGGTACACACCGCGCGGTCCGACGACTACCGCAACCGCCAGGCGGTG 341
Oy 118 GluThrArgValProHisPheGlySerThrAsnSerLeuLeuTrpLeuAsnProAlaGlu 137
    |||||::: |||
Db 342 GAGACCGCGGTCTTCTTCTGGATCCACCGCGGCTTCCGCTACCGCCGACCGACGACGG 401
Oy 138 LysHisIleThrGlyTrpMetAlaProLeuValAspSerLeuGlnLysLeuGlyTrpAla 157
    ::::: |||
Db 402 AGAAATCTTCTG---TACATGGACAAGTTCTGTCCGCGCTGAGCGGCTCGCGTACCGC 458
Oy 158 AspGlyGluThrLeuPheGlyAlaProTyraAspPheArgTrpGlyLeuAlaIleGluGly 177
    |||||::: |||
Db 459 GACCGCGAAGACTGTTCGCGCGCGCTTCCGATCGACTTCGGTACGCGCTCGCCCGCCAGCG 518
Oy 178 HisProSerGlnValGlySerLysPheLeuLysAspLeuLysAsnLeuIleGluGluAla 197
    |||||::: |||
Db 519 CACCGCTCGAGGCTCGCNCAGCGCTTCTTCCGGCGCTCAGAGGCTGTGAGAGAGGCGG 578
Oy 198 SerAsnSerAsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyLeuPhe 217
    |||||::: |||
Db 579 ACCCGGCTAACGAGGAGGAGCGCGGTGACCATTCGTGGCCACAGCACGACGCGCGCACGGTG 638
Oy 218 ValLeuGlnLeuLeuAsnArgAsnProProSerTrpArgLysLysPheIleLysHisPhe 237
    ||| ||| |||
Db 639 GCGGACCACTTCTACTGCGCGCGCGCTTCCGCTGCGCGAGCGGCTTCTCGCGCGCTTC 698
Oy 238 IleAlaLeuSerAlaProTrpGlyGlyAlaIleAspGluMetLysTrpPheAlaSerGly 257
    ::::: |||||
Db 699 GTCGCCGTTGCGCGCGCGCGGTGGAGCGTGTCTTGGCATGTGACATTCGTCCGCGCGG 758
Oy 258 AsnThrLeuGlyValProLeuValAspProLeuLeuValArgAspGluLysSerSer 277
    |||||::: |||
Db 759 AACCATCTTCGCGCTGTCTGTGACCGCGCTGTCAAGGCGCGTACGACGACGCTTG 818
Oy 278 GluSerAsnLeuTrpLeuLeuProAsnProLysIlePheGlyProGlnLysProIleVal 297
    ::|||::: |||
Db 819 CAGAGCAGCTCTGGCGCGCTGCCCAACCCCAACGCATTAGAGCCGCGGACGACCTGGTG 878
Oy 298 IleThrProIleArgProTyrsSerAlaHisAspMetValAspPheLeuLysAspIleGly 317
    ||| ||| |||
Db 879 ACCACACGAGGAGGACGACGACGCGCCACGACATGGCGGACTCTCTCAGCAGCATCGGG 938
Oy 318 PheProGluGlyValTyrrProTyrrGluThrArgIleLeuProLeuIleGlyAsnIleLys 337
    ::|||::: |||
Db 939 CTAGGCGCGCGCAATTCGTGCTGACCAAGTCCCGCTGCTCCCTGTCGGGAGCGCGCA 998
Oy 338 AlaProGlnValProIleThrCysIleMetGlyThrGlyValGlyThrLeuGluThrLeu 357
    ::|||::: |||
Db 999 TCTCCGCGGCTCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1058
Oy 358 PheTyrglyLysGlyAspPheAspGluArgProGluIleSerTyrrGlyAspGlyAspGly 377
    ||| ||| |||
Db 1059 GCGTACCGCGGAGAGCACTTCGACGTGACGCGCGCATGATGTCATGAGAACGCGCGCGG 1118
Oy 378 ThrValAsnLeuValSerLeuLeuAlaLeuGlnSerLeuTrpLysGluGlnLysAsnGln 397
    |||||::: |||
Db 1119 CTGCTCAACCTGTGAGCTCTCTCTGTGACCTCGCTGAGAG---CTTCTTACAGCT 1175
Oy 398 TyrrLeuValValLysIleAspGlyValSerHisThrSerIleLeuLysAspGluVal 417
    ||| ::::: |||
Db 1176 TACTTTAGATCTCAAGGTGCGCAACGTGTCAACACGCGGCTTCTGTTGAGACATGCT 1235

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Oy 418 AlaLeuAsnGluIleValGlyGluIleThrSerIleAsn 430
    |||||::: |||
Db 1236 GCTCTCGCGGTATCATTTAGCGCATCTACGCCCAT 1274
RESULT 9
AAA49205
ID AAA49205 standard; cDNA; 1660 BP.
AC AAA49205;
XX
XX
XX 12-DEC-2000 (first entry)
DE Corn putative lecithin:cholesterol acyltransferase gene #5.
XX
XX
XX Corn; lecithin:cholesterol acyltransferase; phytosterol;
KW phosphatidylcholine-sterol O-acyltransferase; heat shock; cold shock; ss.
XX
XX Zea mays.
XX
XX
XX Key Location/Qualifiers
XX CDS 77..1396
XX FT /tag= a
XX FT /product= "lecithin:cholesterol acyltransferase"
XX FT /EC_number= "2.3.1.43"
XX
XX WO200032791-A2.
XX
XX 08-JUN-2000.
XX
XX 02-DEC-1999; 99WO-US28586.
XX
XX 03-DEC-1998; 98US-0110782.
XX
XX (DUP0 ) DU PONT DE NEMOURS & CO E. I.
XX
XX Cahoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;
XX WPI; 2000-412337/35.
XX DR P-PSDB; AAB01210.
XX
XX Polynucleotide encoding plant lecithin:cholesterol acyltransferase
XX enzyme useful for producing transgenic plants and for producing
XX PT antibodies specific to which is useful for screening cDNA expression
XX PT libraries.
XX
XX Claim 2; Page 43-44; 49pp; English.
XX
XX The present sequence is a putative coding sequence for a corn
XX CC lecithin:cholesterol acyltransferase (also known as
XX CC phosphatidylcholine-sterol O-acyltransferase). This enzyme is found
XX CC associated with high-density lipoproteins and Apolipoprotein-AI and
XX CC The gene and protein can be used to produce transgenic plants which have
XX CC increased lipid metabolism and membrane fluidity, and therefore increased
XX CC resistance to heat and/or cold shock, to alter the content of phytosterol
XX CC or lecithin in grains and to identify potential herbicides.
XX
XX SQ Sequence 1660 BP; 361 A; 475 C; 499 G; 325 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 2,93e-69 Length: 1660
XX Score: 739.50 Matches: 171
XX Percent Similarity: 60.10% Conservative: 76
XX Best Local Similarity: 41.61% Mismatches: 141
XX Query Match: 31.70% Indels: 23
XX DB: 21 Gaps: 15
XX
XX US-09-857-612A-14 (1-443) x AAA49205 (1-1660)
Oy 33 AlaSerAsnLeuAspProIleLeuIlePheProGlyAsnGlyLysGlnLeuGluAla 52
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Db 179 GCCACACACTTCCACCCCATCTTCTGTGAGTGGGCTGACGTGACGACCTGAGGCA 238
Oy 53 ArgLeuThrAsnGlnTyrrLysProSerThrPheIleCysGluSerTrpTyProLeuIle 72

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Db 239 CGCCTCACCGAGAGTACCGCCCTCGTCCGACCTCGCGCC----- 283
 Oy 73 LysLysAsnGlyTTPheArgLeuTriPheAspSerValIleLeuAla---Pro 91
 Db 284 ATGAAGGAGGAAGGGGTGCTGCTGTGGAAGACAGTGTGAGAGCTGTCTGTGAC 343
 Oy 92 PheThrIncysPheAlaGluArgMetThrLeuHisTyrHisGlnGluLeuAspPtyr 111
 Db 344 TACGTGAGTGTCTCGAGGAGACATAGACCTCTACGACCCCTGCATACAGAGTAC 403
 Oy 112 PheAsnThrProGlyValGluThrArgValProHisPheGlySerThrAsnSerLeu 131
 Db 404 CGAACTCCGCGCGTGCAGACCGAGTGCCTCACTTCGCTCCACAGACCTTCAGC 463
 Oy 132 TyrLeuAsnProArgLeuHisIleThrGlyTyrMetAlaProLeuValAspSerLeu 151
 Db 464 CACAAAGAACCC---CTCAAGTCA---GACTGTGCTCGGAAAGCTGAGACCGCACTG 517
 Oy 152 GlnLysLeuGlyTyrAlaAspGlyGluThrLeuPheGlyAlaProTyrAspPheArgTyr 171
 Db 518 GAACACATGGAGATACCGAGACGAGACACCATTTCCGAGGCCCTTACGACTTCCTGAC 577
 Oy 172 GlyLeuAlaAlaGluGlyHisProSerGluValGlySerLysPheLeuLysAspLeuLys 191
 Db 578 GCGCGCGCGTCCCGCGCAGACGTCGAGGTGACTCCCGCTACTTCAGAGAGCTGATG 637
 Oy 192 AsnLeuIleGluGluAlaSerAsnSerAsnGlyLysProValIleLeuLeuSerHis 211
 Db 638 GAGCTGTGTGCGAGCGGAGGAGAGACCGGAAAGAGCGGCTCATC---CTGCGGCAC 694
 Oy 212 SerLeuGlyGlyLeuPheValLeuGlnLeuAsnArgAsnProProSerTyrArgLys 231
 Db 695 AGCTTCGCGCGCATGCTCGCTGAGTGTCTCGGAAACACTCCGCGCGCTGCGCGGC 754
 Oy 232 LysPheIleLysHisPheIleAlaLeuSerAlaProTyr-----GlyGlyAlaIleAsp 249
 Db 755 GAGACATCGAGCGCGCTGCTC---CTGTGCGCGCAGCGCTCCCGCGGCTTCTGTGAG 811
 Oy 250 GluMetTyrThrPheAlaSerGly---AsnThrLeuGlyValProLeuValAspProLeu 268
 Db 812 CCGGTGTGCAACTTCGCGTCCGCGAGCAGACATCTTACGTCAGCAGCAGCGCGCTG 871
 Oy 269 LeuValArgAspGluGlnArgSerSerGluSerAsnLeuThrLeuProAsnProLys 288
 Db 872 GCCACGGGAGCATGTGAGAGAGCTTCGAGAGCGCCCATGTAATTCCCTCGCGCGC 931
 Oy 289 IlePheGlyPro---GlnLysProIleValIleThrProIleArgProTyr-----Ser 305
 Db 932 GTCTTCGGGCGCCCTGCAAGCGCGCTGTGTGTACACAGGAGCGGAATCTCCGCGTCC 991
 Oy 306 AlaHisAspMetValAspPheLeuLysAspIleGlyPheProGluGlyValTyrProTyr 325
 Db 992 GCGCAGACATGTGAGCGCTTCTCGCGCGCTCCGCGTCCGCGAGCGCGCGACCTTTC 1051
 Oy 326 GluThrArgIleLeuProLeuIleGlyAsnIleLysAlaProGlnValProIleThrCys 345
 Db 1052 AGGAGAGCGCGCGTCCCAAGATGAGGCTTCGCGCGCGAGTGTGCCATGACGATAC 1111
 Oy 346 IleMetGlyThrGlyValGlyThr---LeuGluThrLeuPheTyrGlyLysGlyAspPhe 364
 Db 1112 ATCAGCGGGGTGCGCAACAGACGCGCTGCGGTGTCTGCGGAG---GACTTC 1168
 Oy 365 AspLysArgProGluIle---SerTyrGlyAspGlyLysAspGlyThrValAsnLeuValSer 383
 Db 1169 GACCGCGCGCGAGGAGGTGCGCGCTACGAGCGAGATGCAAGATCAATTTGATGACG 1228
 Oy 384 LeuLeuAlaLeuGlnSerLeuTyrLys-----GluGluLysAsnGlnTyrLeuLys 400
 Db 1229 GTCTTCGCGTTCGAAAGAGAGATGCTGCGGACCGGAGCAGAAAGACAGTTC---AAA 1285
 Oy 401 ValValLysIleAspGlyValSerHisThrSerIleLeuLysAspGluValAlaLeuAsn 420

Db 1286 TCATCAAGATCAATAGCCAGCATTTACATGCTACAGGATGATTTGCCCTGCAC 1345
 Oy 421 GluIleValGlyGluIleThrSerLeuAsnSer 431
 Db 1346 AGGCTATTCAAGAAATTGTTGAGGCCAATTAAT 1378
 RESULT 10
 ID AAA49203
 AAA49203 standard; cDNA: 1440 BP.
 AC AAA49203;
 XX 13-DEC-2000 (first entry)
 DE corn putative lecithin:cholesterol acyltransferase gene #3.
 XX KW Corn; lecithin:cholesterol acyltransferase; phytoesterol;
 XX KM phosphatidylcholeline-sterol O-acyltransferase; heat shock; cold shock; ss.
 XX OS Zea mays.
 FH Key Location/Qualifiers
 FT CDS 19..1323
 FT /tag= a
 FT /product= "lecithin:cholesterol acyltransferase"
 FT /EC_number= "2.3.1.43"
 PN W0200032791-A2.
 XX 08-JUN-2000.
 PD 02-DEC-1999; 99WO-US28586.
 PF 03-DEC-1998; 98US-0110782.
 PR (DUP0) DU PONT DE MEMOURS & CO E I.
 PA Canoon RE, Kinney AJ, Sakai H, Shen JB, Butler KH, Saylor JJ;
 DR WPI: 2000-412337/35.
 DX P-PSDB; AAB01208.
 XX PT Polynucleotide encoding plant lecithin:cholesterol acyltransferase
 PT enzyme useful for producing transgenic plants and for producing
 PT antibodies specific to which is useful for screening cDNA expression
 PT libraries
 PS Claim 2; Page 39-40; 49pp; English.
 PS XX
 CC The present sequence is a putative coding sequence for a corn
 CC lecithin:cholesterol acyltransferase (also known as
 CC phosphatidylcholeline-sterol O-acyltransferase). This enzyme is found
 CC associated with high-density lipoproteins and Apolipoprotein-AI and -D.
 CC The gene and protein can be used to produce transgenic plants which have
 CC increased lipid metabolism and membrane fluidity, and therefore increased
 CC resistance to heat and/or cold shock, to alter the content of phytosterol
 CC or lecithin in grains and to identify potential herbicides.
 CC XX
 SO Sequence 1440 BP; 273 A; 474 C; 440 G; 253 T; 0 other;
 Alignment Scores:
 Pred. No.: 6,24e-67 Length: 1440
 Score: 717.00 Matches: 160
 Percent Similarity: 55.97% Conservative: 65
 Best Local Similarity: 39.80% Mismatches: 161
 Query Match: 30.73% Indels: 16
 DB: 21 Gaps: 8
 US-09-857-612a-14 (1-443) x AAA49203 (1-1440)
 Oy 36 LeuAspProLeuIleLeuIleProGlyAsnGlyLysGlnLeuGluAlaArgLeuThr 55
 Db 136 CTCACCGCGTGTGTGTGTGCGCGGCTGACGTGACAGCAGAGCTGTGACGCGCGCTCACG 195

OY	56	AsnGlnTyrLysProSerThrPheIleCysGlnSerTrpTrpProLeuIleLysLysLys	75
Db	196	GACGGCTACGCCCCCTTCGCGCCCGCTGGGAT-----GAGGG	234
OY	76	AsnGlyTrpPheArgLeuTrpPheAspSerSerValIleLeuAla---ProPheThrGln	94
Db	235	GAAAGCGGTGTTCGGCTCTGGTACCACACTGCTCCGACTCCGCCACACACTGCGGG	294
OY	95	CysPheIleAlaGluArgMetThrLeuHisLysGlnGluLeuAspArgTrpPheAsnThr	114
Db	295	TGCTTCATGGAGCAAGATGGCCCTGTATACGACCCCGTGGCCGACACACTACCGGAACCTG	354
OY	115	ProGlyValIleGluThrArgValProHisPheGlySerThrAsnSerIleuLeuTyrLeuAsn	134
Db	355	CCCGCGCTCGAGACGGCCGTCGTCGCAATTTGGCTCTCCCGAGACA---TTCCAGAAAGAAC	411
OY	135	ProArgLeuLysHisIleThrGlyTyrMetAlaProLeuValAspSerIleuLysLysLys	154
Db	412	CCGGAGCACACGACCTGGTCTCTGGTCTTCAGAGCTCTCAGAAACAGATGGCAAGGCC	471
OY	155	GlyTyrAlaAspGlyLeuThrLeuPheGlyAlaProTyrAspPheArgTyrGlyLeuAla	174
Db	472	GGGTACCGCGACGGCGACACCTGTGGGGGCCCGGTACGACCTCCGCTACGCCCGCGCG	531
OY	175	AlaGluGlyHisProSerGlnValGlySerLysPheLeuLysAspLeuLysAsnLeuIle	194
Db	532	GTGGCGCGCCAGCATGAGAGTCTTCGCGCTACTTCGTCGGCGCTGGCGCGCCGCTCTGTC	591
OY	195	GluGluAlaSerAsnSerAsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGly	214
Db	592	GAGAGCGCGACGCCCAAGAACCGGGCGAGGAAGTATCTCTTCGGCGACACTTCCGGG	651
OY	215	GlyLeuPheValIleuGlnLeuLeuLeuAsnArgAsnProProSerTrpArgLysLysPheIle	234
Db	652	GGCATGTGGTGGCGGTGGATTCGTCCGAGACACTCCATGGCGGGGAGACAGTATATC	711
OY	235	LysHis---PheIleAlaLeuSerAlaProTrpGlyAlaIleAspIleuMetYrThr	253
Db	712	AAGCACTCTTCCTCTGTCGCCCCGGTGGCCGGAGAGGTTGCTGAAGCCGCTGCAAGTAC	771
OY	254	PheAlaSerGly---AsnThrLeuGlyValIleProLeuValAspProLeu-----LeuVal	270
Db	772	TTTCGCTCCGGGTCCAACTGATGATACGTCCGACAGTCACTGATCGGTGACGCTCTT	831
OY	271	ArgAspGluGlnArgSerSerGlySerAsnLeuTrpLeuLeuProAsnProLysIlePhe	290
Db	832	AGGCGCATGTGGCGACCTTCGATGCTCTCTCTGTCACCTCCCTCCACCGGCTGTTCC	891
OY	291	GlyProGlnLysProIleValIleThrProIleArgProTyrSerAlaHisAspMetVal	310
Db	892	GGG---CGCAGCGCGCTCGTGTCAACCGCGGAGGAACACTACTCCGCTTACGACCTGGAG	948
OY	311	AspPheLeuLysAspIleGlyPheProGluGlyLysTrpProTyrGlnThrArgIleLeu	330
Db	949	GACCTCTCTGCTCGCCCTCGCTGACGCGCGCGGTGGAACCTTGAGAGAGAGCGCGCTC	1008
OY	331	ProLeuIleGlyAsnIleLysAlaProGlnValProIleThrCysIleMetCysIleThrLys	350
Db	1009	CCCAAGATGAGACTACTTCCACGGGCCCAAGTGTGTCGACACACTGATGAGACGGGTGGCG	1068
OY	351	ValGlyThrLeuGlnThrLeuPheTyrGlyLysGlyAspPheAspGluArgProIleLys	370
Db	1069	AACGACACGCGCGAGACGCTCGTCTACTGGAGCGGCACTTGGACCGCACCCCGAGATA	1128
OY	371	SerTyrGlyAspGlyAspGlyThrValAsnLeuValSerLeuLeuAlaLeuGlnSerLeu	390
Db	1129	GTTGTACGCGCAGCGGCGCAATTTCCATCAATTTGGTCAGCATCTGCGCTTGACAGAGAAG	1188
OY	391	TrpLysGlu-----GluLysAsnGlnTyrLeuLysValValLysIleAspGlyValSer	408
Db	1189	ATGCGCGCGCAGCGCGGAAACAAAGAGGTGTACAAAGTGCATGAATAATTTCTGTGGCGCCAG	1248

Oy	409	HsHrHsrILeLeuLysAspGluValAlaLeuAsnGluIleValAlcYgluIleHrSer	428
Db	1249	CACGGTACTATTGTGCACACGACGACGCGCCCTCAACGGGCTCATGCACGAATCTCTGA	1308
Oy	429	Ileasn	430
Db	1309	GCGAAT	1314
RESULT 11			
ID	AAV68568	standard; cDNA; 1236 BP.	
XX	AAV68568;		
XX	16-FEB-1999	(first entry)	
DE	Murine kidney lecithin-cholesterol acyltransferase-1-like gene.		
KW	Murine; kidney; lecithin-cholesterol acyltransferase-1-like protein;		
KW	LCAT; agonist; arteriosclerosis; atherosclerosis; hyperlipidemia;		
KW	atherosclerosis hypercalorism; obesity; hypertriglyceridemia;		
KW	inflammatory disease; senescence; renal disorder; inhibition;		
KW	malnutrition; abetalipoproteinemia; inflammatory disease;		
XX	Tangier disease; ds.		
OS	Mus sp.		
XX			
FE	Key	Location/Qualifiers	
FT	CDS	1..1236	
FT		/*lag= a	
FT		/product= "LCAT protein"	
XX			
PN	W09846767-A1.		
PD	22-OCT-1998.		
XX			
PE	09-APR-1998; 98WO-JP01643.		
XX			
PR	22-JAN-1998; 98JP-0010289.		
PR	11-APR-1997; 97JP-0093355.		
PR	10-JUL-1997; 97JP-0184885.		
XX			
PA	(TAKE) TAKEDA CHEM IND LTD.		
XX			
PI	Taniyama Y;		
XX			
DR	WPI: 1998-594583/50.		
XX	P-PSDB; AAW80944.		
PT	Isolated lecithin-cholesterol acyltransferase proteins - used to		
PT	develop products for treating e.g. atherosclerosis, obesity,		
PT	inflammatory diseases, senescence, diseases of the brain or renal		
PT	disorder.		
XX			
SS	Claim 7; Pages 146-147; 190pp; English.		
XX			
CC	This is the nucleotide sequence encoding a novel murine kidney		
CC	lecithin-cholesterol acyltransferase-like protein, used in the method		
CC	of the invention. The novel proteins have LCAT-like activity. The		
CC	proteins and agonists can be used for treating or preventing e.g.		
CC	arteriosclerosis, atherosclerosis, hyperlipidemia, atherosclerosis		
CC	hypercalorism, obesity, hypertriglyceridemia, inflammatory diseases,		
CC	senescence, diseases of the brain, or renal disorder. Inhibitors of		
CC	the protein can be used for treating or preventing e.g. malnutrition,		
CC	abetalipoproteinemia, inflammatory diseases, Tangier disease		
CC	(analphalipoproteinemia) and other diseases. The products can also be		
CC	used for detection, diagnosis and drug screening as part of a kit.		
XX			
SQ	Sequence 1236 BP; 269 A; 342 C; 348 G; 277 T; 0 other;		

Alignment Scores:

Pred. No.: 9,68e-56

Score: 612.00

Length: 1236

Matches: 139

[illegible]

Db	955	GAAGCAATGAGCCAGCCACCCGGGCTGAGACCTGACTGCTTGATGGCAGCTGGTCTCCACG	1014
Qy	354	LeuGIuThrLeuPheTyrGlyGlyAspPheAspGluArg---ProGluIleSerTyr	372
Db	1015	CCAAACCTCTTCTTCACTAC-----GAGAGCTTTCCTGATCGGAGACCCAAATCTGCTTC	1068
Qy	373	GlyAspGlyAspGlyThrValAsnLeuValSerLeuLeuAlaLeuGlnSerIleuTrpLys	392
Db	1069	GCCGATGGTGTGACGGCAGCGTGAACCTGGAGAGCGTCTCTCAGTGCACAGCC--TGGCAG	1125
Qy	393	GIuGIuLysAsnGlnTyrIleLysValValIleAspGlyValSerHisThrSerIle	412
Db	1126	AGCCGCCAAGGACGACAGATGATCATTTGCAGAGACTGCCGGGAAGCGACATTTGAGATG	1185
Qy	413	LeuLysAspGIuValAlaLeu	419
Db	1186	CTAGCCATGCGCACCACTTG	1206
RESULT 12			
AAV68566			
ID	AAV68566	standard; cDNA; 1236 BP.	
XX	AAV68566;		
AC	AAV68566;		
XX	16-FEB-1999	(first entry)	
DT	16-FEB-1999	(first entry)	
XX	Human heart	lecithin-cholesterol acyltransferase-like gene 3.	
DE	Human heart	lecithin-cholesterol acyltransferase-like gene 3.	
XX	Human; heart; lecithin-cholesterol acyltransferase-like protein;		
KW	LCAAT; agonist; arteriosclerosis; atherosclerosis; hyperlipidemia;		
KW	atherosclerosis hypercalorism; obesity; hypertiglyceridemia;		
KW	inflammatory disease; senescence; renal disorder; inhibition;		
KW	malnutrition; abetalipoproteinemia; inflammatory disease;		
KW	Tangier disease; ds.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FH	CDS	1..1236	
FT		/*tag= a	
FT		/product= "LCAAT protein"	
XX	MO9846767-AI.		
PN	22-OCT-1998.		
XX	22-OCT-1998.		
PD	09-APR-1998;	98MO-JP01643.	
XX	09-APR-1998;	98MO-JP01643.	
PF	22-JAN-1998;	98JP-0010289.	
XX	22-JAN-1998;	98JP-0010289.	
PR	11-APR-1997;	97JP-0093355.	
XX	11-APR-1997;	97JP-0093355.	
PR	10-JUL-1997;	97JP-0184885.	
XX	10-JUL-1997;	97JP-0184885.	
XX	(TAKE) TAKEDA CHEM IND LTD.		
PA	(TAKE) TAKEDA CHEM IND LTD.		
XX	Tanlyama Y;		
PI	WPI; 1998-594583/50.		
XX	WPI; 1998-594583/50.		
DR	P-PSDB; AAM80942.		
XX	P-PSDB; AAM80942.		
XX	Isolated lecithin-cholesterol acyltransferase proteins - used to		
PT	develop products for treating e.g. atherosclerosis, obesity,		
PT	inflammatory diseases, senescence, diseases of the brain or renal		
PT	disorder.		
XX	Example 1; Pages 144-145; 190pp; English.		
PS	Example 1; Pages 144-145; 190pp; English.		
XX	This is the nucleotide sequence encoding a novel human heart		
CC	lecithin-cholesterol acyltransferase-like protein, used in the method		
CC	of the invention. The novel proteins have LCAAT-like activity. The		
CC	proteins and agonists can be used for treating or preventing e.g.		
CC	arteriosclerosis, atherosclerosis, hyperlipidemia, atherosclerosis		
CC	hypercalorism, obesity, hypertiglyceridemia, inflammatory diseases,		
CC	senescence, diseases of the brain, or renal disorder. Inhibitors of		

CC the protein can be used for treating or preventing e.g. malnutrition,
 CC abetalipoproteinemia, inflammatory diseases, Tangle disease
 CC (abetalipoproteinemia) and other diseases. The products can also be
 CC used for detection, diagnosis and drug screening as part of a kit.

XX Sequence 1236 BP; 247 A; 381 C; 359 G; 249 T; 0 other;

Alignment Scores:

Pred. No.:	1,59e-55	Length:	1236
Score:	610.00	Matches:	141
Percent Similarity:	54.57%	Conservative:	80
Best Local Similarity:	34.81%	Mismatches:	156
Query Match:	26,15%	Indels:	28
DB:	19	Gaps:	12

US-09-857-612A-14 (1-443) x AAV68566 (1-1236)

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QY 21 ValValValMetLeuSerLeuLeuLys-----ThrcysGlyAlaSerAsnLeuAspPro 38
DB 58 CTCTCTGCTGCTAAATGCTGCTGCGGAGCCAGCCCTCCGGCCGAGCTCAACCCCA 117
QY 39 LeuLeuLeuLeuProGlyAsnGlyGlyAsnGlnLeuGlnValArgLeuThrAsnGlnTyr 58
DB 118 GTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 168
QY 59 LysProSerThr-----PheLeuGlySerThrTyrProLeuLeuLysLysAsn 76
DB 169 AACCCGACAGTGGTGCATCTCTCTCTC-----AAGAGACCGAA 210
QY 77 GlyTyrPheArgLeuThrPheAspSerSerValIleLeuAlaProPheThrGlnCysPhe 96
DB 211 AGCTACTCTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 270
QY 97 AlaGluArgMetThrLeuLeuIleTyrGlnGlnLeuLeuAspArgTyrPheAsnThrProGly 116
DB 271 ATTGACAAATATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 330
QY 117 ValGluThrArgValProHisPheGlySerThrAsnSerLeuLeuTyrLeuAsnProArg 136
DB 331 GTGAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 390
QY 137 LeuLysHisIleLeuThrGlyTyrMetAlaProLeuValAspSerLeuLysLeuGlyTyr 156
DB 391 AAAAGCAGCGTGGCTTCATTTTCCACACCATTGCTGAGAGCTTGTGGCTGGCTGCTAC 450
QY 157 AlaAspGlyGluThrPheArgPheGlyAlaProTyrAspPheArgTyrGlyLeuAlaGlu 176
DB 451 AACAGGGGTGAGATGCTGCGAGGGCTCCCTATGACTGGCGCGAGCC-----498
QY 177 GlyHisProSerGlnValGlySerLysPheLeuLysAspLeuLysAsnLeuIleGln 196
DB 499 -----CAAATGAAAGAGGGCTCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
QY 197 AlaSerAsnSerAsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyLeu 216
DB 550 ATGTACCACTGTATGGGGG---CCCGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
QY 217 PheValLeuGlnLeuLeuAsnArgAsnProProSerThrArgLysPheIleLysHis 236
DB 607 TACAGCTCTACTTTTGCAGCGCGAGCGGAGCTTGAAGAGACAATATATCCGGCC 666
QY 237 PheIleAlaLeuSerAlaProTyrGlyGlyAlaIleAspGluMetLysThrPheAlaSer 256
DB 667 TTCGTGTCACTGGTGGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCA 726
QY 257 GlyAsnThrLeuGlyAlaProLeuValAspProLeuLeuValArgAspGlnArgSer 276
DB 727 GGAGACAAACACCGGATCCAGTCAATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGTCA 786
QY 277 SerGluSerAsnLeuThrLeuLeuProAsnProLysIlePheGlyProGlnLysProIle 296
DB 787 GCTGTCTCCACAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846

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QY 297 ValIleThrProIleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIle 316
DB 847 GTCCAGACACCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 906
QY 317 GlyPheProGlnGly---ValTyrProTyrGluThrArgIleLeuProLeuIleGlnAsn 335
DB 907 GGCCTTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 336 IleLysAlaProGlnValProIleThrCysIleMetGlyThrGlyValGlyThrLeuGln 355
DB 961 ACGATGCACCTGGCGGCGGAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 356 ThrLeuPheTyrGlyLysGlyAspPheAspGluArg---ProGluIleSerTyrGlyAsp 374
DB 1021 TCCCTTACTAT-----GAGACCTTCCCTGACCGCTGACCTGAAATCTGCTTGGTGAC 1074
QY 375 GlyAspGlyThrValAsnLeuValSerLeuAlaLeuGlnSerLeuThrLysGlnGlu 394
DB 1075 GGCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1131
QY 395 LysAsnGlnTyrLeuLysValValLysIleAspGlyValSerHisThrSerIleLeuLys 414
DB 1132 CAGGACACCAATGTTGCTGCGAGAGCTGCGACGAGCAGCAGCAGCAGCAGCAGCAGCAGC 1191
QY 415 AspGluValAlaLeu 419
DB 1192 AACGCCACCACTCTG 1206

RESULT 13
AA234023
ID AA234023 standard; cDNA; 2680 BP.
XX
AC AA234023;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO540 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PE 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.

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31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 21-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082766.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083332.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 18-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 30-JUL-1998; 98US-0087208.
PR 11-SEP-1998; 98US-0094651.
PR 98US-0100038.
PA (GETH) GENENTECH INC.
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI, 1999-551358/46.
XX P-PDB; AA41708.

PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
XX
XX
PS Claim 2; Fig 58; 530pp; English.
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA34338, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 2680 BP; 518 A; 800 C; 782 G; 580 T; 0 other;

Alignment Scores:
Pred. No.: 4,98e-55 Length: 2680
Score: 610.00 Matches: 141
Percent Similarity: 54.57% Conservative: 80
Best Local Similarity: 34.81% Mismatches: 156
Query Match: 26.15% Indels: 28
DB: Gaps: 12

US-09-857-612A-14 (1-443) x AA234023 (1-2680)
QY 21 ValValValMetLeuSerLeuLeuCyS-----ThrcysGlyAlaSerAsnLeuAspPro 38
Db STCTTGCTGCTGCTATATCTGCTGCTGCGGACCCAGCCGCTCCGCGGCGGACGTCACCCCA 137
QY 39 LeuLeuLeuLeuProGlyAsnGlyAlaGlnGlnLeuGlnAlaArgLeuThrAsnGlnIntyr 58
Db GTGGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 138
QY 59 LysProSerThr-----PheIleCysGluSerTyrTyrProLeuIleLysLysAsn 76
Db AAGCGGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 189
QY 77 GlyThrPheArgLeuThrPheAspSerSerValIleLeuAlaProPheThrGlnCysPhe 96
Db AGCTACTTCACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 231
QY 97 AlaGluArgMetThrLeuHisIleThrHisGlnIleuAspAspTyrPheAsnThrProGly 116
Db ATTGACATATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 291
QY 117 ValGluThrArgValProHisPheGlySerThrAsnSerLeuLeuTyrLeuAsnProArg 136
Db GTGATGTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 351
QY 137 LeuLysHisIleThrGlyTyrMetAlaProLeuAlaAspSerLeuGlnLysLeuGlyTyr 156
Db AAAAGCAGCGTGGGCTCTTATTCACACACATGGGAGAGCTGTGTGGCTGGGCTGAC 411
QY 157 AlaAspGlyGluThrLeuPheGlyAlaProTyrAspPheArgTyrGlyLeuAlaGln 176
Db ACACGGGCTGAGATGTCGAGGGGCTCCATATGCTGCGCGAGCC----- 471
QY 177 GlyHisProSerGlnValGlySerLysPheLeuLysAspLeuLysAsnLeuIleGln 196
Db -----CCAAATGAAGAACGGGCTCTACTCTCTGCGC-----CTCCCGGAGATATCATGAGAG 519
QY 197 AlaSerAsnSerAsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyGly 216
Db ATGTACACAGCTGTATGGGGC-----CCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 570
QY 217 PheValLeuGlnLeuLeuAsnArgAsnProProSerTyrPArgLysLysPheIleLysHis 236
Db TACACGCTCTTCTTCTGACGCGGAGCGGAGCGGCTGTGAAGACAAATATATCCGGGCC 627

QY 137 LeulysHisIleThrglyTYrMetAlaProLeuValAspSerLeuGlnLysLeuGlyTYr 156
 Db 411 AAAGCAGCGTGGTCTATTCACACACATGGTGGAGAGCTTGTGGCTGGGGCTAC 470
 QY 157 AlaSpGlyGluThrLeuPheGlyAlaProTyrTrpAspPheArgTYrGlyLeuAlaActu 176
 Db 471 ACACGGGGGTGAGATGCCGAGGGGCTCCATATGACTGCGCCGAGCC----- 518
 QY 177 GlyHisProSerGlnValGlySerLysPheLeuLysAspLeuLysAsnLeuIleGlu 196
 Db 519 -----CCAATGAAACAGGGCCCTACTCTCTGGCC---CTCCGGAGATATATCAGAGAG 569
 QY 197 AlaSerAsnSerAsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyLeu 216
 Db 570 ATGATACAGCTGTATGGGGGCG---CCCGTGGTGGTGGTGGCCACAGATATGGGCAACTG 626
 QY 217 PheValLeuGlnLeuLeuAsnArgAsnProProSerTTPArgLysLysPheIleHis 236
 Db 627 TACACGCTCTACTTCTGACAGCGCAGCGCAGCGCTGGAAGGAGCAACTATATCGGGCC 686
 QY 237 PheIleAlaLeuSerAlaProTyrGlyValAlaIleAspGluMetTYrThrPheAlaSer 256
 Db 687 TTCCTGTACACTGGGTGGCCCTGGGGGGGCGTGGCCAAAGACCTGGCGCTCTCA 746
 QY 257 GlyAsnThrLeuGlyValProLeuValAspProLeuLeuValArgAspGlyGlnArgSer 276
 Db 747 GGAGACAAACACGCGATCGCATCGGGCGCCCTGAAGATCCGGAGACACAGGGGCA 806
 QY 277 SerGluSerAsnLeuThrLeuLeuProAsnProLysIlePheGlyProGlnLysProIle 296
 Db 807 GCTGTCTCCACACCTGCTGCTGCTCCATCAACATACATGTCGACCTGAGAGAGCTTTC 866
 QY 297 ValIleThrProIleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIle 316
 Db 867 GTGCAGACACCCCAATCACTACACACTCGGGGAGCTACCCCAAGTTTCTCAGGACATC 926
 QY 317 GlyPheProGluGly---ValTyrProTyrGlyThrArgIleLeuProLeuIleGlyAsn 335
 Db 927 GCGTTTGAAATGGCTGGCTCATCGCGGAGACACAGAA-----GGCGTGGTGAAGCC 980
 QY 336 IleLysAlaProGlnValProIleThrcysIleMetGlyThrGlyValGlyTYrLeuGlu 355
 Db 981 ACGATGCCACCTGCGTGCACCTGACCTCATGTGCTGCGCTGCCACACACACAC 1040
 QY 356 ThrLeuPheTyrGlyLysGlyAspPheAspGluArg---ProGluIleSerTYrGlyAsp 374
 Db 1041 TCCCTTCTACTAT-----GAGAGCTTCCCTGACCGTACCTAAATCTGCTTGGTAC 1094
 QY 375 GlyAspGlyThrValAsnLeuValSerLeuLeuAlaLeuGlnSerLeuTrpLysGlu 394
 Db 1095 GGCATGGTACTGTGAAGCTTAAGAGTCCCTGCAGTCCAGGCC---TGGCAGAGCCGC 1151
 QY 395 LysAsnGlnTyrLeuLysValValLysIleAspGlyValSerHisThsSerIleLeuLys 414
 Db 1152 CAGGAGCACCAGTGTGCTGTCAGAGAGCTCCAGGACGACGACATGAGATGCTGGCC 1211
 QY 415 AspGluValAlaLeu 419
 Db 1212 AACGCCACACCGCTG 1226
 RESULT 15
 ID AAA88516 standard; cDNA; 2680 BP.
 AC AAA88516;
 XX 22-JAN-2001 (first entry)
 DE Human PRO540 cDNA clone DNA44189-1322.
 KW PRO540; human; ocular disease; retinopathy; maculopathy; therapy;
 KW retinitis pigmentosa; macular degeneration; retinal detachment;
 KW retinal tear; macular hole; myopia; traumatic choriorretinopathy;

KW acute retinal necrosis syndrome; contusion; edema;
 KW retinal vision occlusion; vascular disease; retinal vasculitis;
 KW thrombocytopenic purpura; uveitis; retinal occlusion; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 21..1259
 FT sig_peptide /*tag= a
 FT 21..104
 FT mat_peptide /*tag= b
 FT 105..1256
 FT /*tag= c
 PN WO200053760-A2.
 XX 14-SEP-2000.
 PD 10-MAR-2000; 2000WO-US06319.
 PP 12-MAR-1999; 99US-0123957.
 PR (GETH) GENENTECH INC.
 PA Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC;
 PI Klein RD, Kijavlin IJ, Kuo SS, La Fleur M, Wood WT;
 XX WP1: 2000-587437/55.
 DR P-PSDB: AAB19579.
 XX
 PT Novel PRO polypeptides useful for preventing or rescuing retinal cells
 PT from injury caused by ocular diseases such as retinitis pigmentosa,
 PT retinopathy, retinal degenerative diseases, degenerative myopia,
 PT uveitis -
 XX
 PS Example 10: Fig 3; 140bp; English.
 SS
 CC The present sequence is that of cDNA clone DNA44189-1322 or UNQ341
 CC (ATCC 209699) isolated from a human foetal tissue cDNA library
 CC using primers and probes (see AA88527-29) based on a consensus (see
 CC AA88522) of sequences obtained from expressed sequence tag databases
 CC using secreted protein extracellular domains. The clone contains a
 CC single open reading frame encoding a 412-amino acid protein (see
 CC AAB19579) designated PRO540. The isolated cDNA can be used in the
 CC recombinant production of PRO540. The invention relates to the
 CC use of PRO polypeptides, including PRO540, to delay, prevent
 CC or rescue retinal cells such as retinal neurons selected from
 CC photoreceptors, retinal ganglion cells, displaced retinal ganglion
 CC cells, amacrine cells, displaced amacrine cells, horizontal and
 CC bipolar neurons, and supportive cells (including Mueller cells and
 CC pigment epithelial cells) from injury and degradation. The retinal
 CC cells are preferably photoreceptors and photoreceptor cell injury or
 CC death is caused by retinal injury, light or environmental trauma or
 CC by an ocular disease selected from retinitis pigmentosa, macular
 CC degeneration, including age-related, retinal detachment, retinal
 CC tears, retinopathy, retinal degenerative diseases, macular holes,
 CC degenerative myopia, acute retinal necrosis syndrome, traumatic
 CC choriorretinopathies or contusion such as Purtscher's retinopathy,
 CC edema, ischemic conditions such as central or branch retinal vision
 CC occlusion, collagen vascular diseases, thrombocytopenic purpura,
 CC uveitis, retinal vasculitis and occlusion associated with Fales
 CC disease and systemic lupus erythematosus (claimed).
 CC
 XX
 SQ Sequence 2680 BP; 518 A; 800 C; 782 G; 580 T; 0 other;
 Alignment Scores:
 Pred. No.: 4.98e-55 Length: 2680
 Score: 610.00 Matches: 141
 Percent Similarity: 54.57% Conservative: 80
 Best Local Similarity: 34.81% Mismatches: 156
 Query Match: 26.15% Indels: 28
 DB: 21 Gaps: 12

US-09-857-612A-14 (1-443) x AAA88516 (1-2680)

Oy	21	ValValValMetLeuSerLeuLeuCys-----ThcysLysAlaSerLysLeuAspPro	38
Db	78	CTCTTCGCTGCTGCTAAATGCTGCTCTCGCGAGCCACAGCCTCCCGGCCGAGCTCACCCCCCA	137
Oy	39	LeuLeuLeuLeuProGlyAsnGlyGlyAsnGlnLeuGlnValaArgLeuThrAsnGlnTyr	58
Db	138	GTGGGCTGCGTCCCTGGTGATTTGGTAACCACTGGAAAGCCAAAGCTGGAC-----	188
Oy	59	LysProSerThr-----PheIleCysGlnSerTrpTyrProLeuIleLysLysAsn	76
Db	189	AAAGCGAGAGTGGTGCACCTACTGCTGCTCC-----AAGAAGACCGAA	230
Oy	77	GlyTrpPheArgLeuTrpPheAspSerSerValIleLeuAlaProPheThrGlnCysPhe	96
Db	231	AGCTACTTCACAAATCTGGCTGGACCTGGACCTGCTGCTGCTCATTCATGACTGCTGG	290
Oy	97	AlaGluArgMetThrLeuAlaHisTyrHisGlnLeuAspAspTyrPheAsnThrProGly	116
Db	291	ATTGACATATACAGCTGCGTGTTCACAAACAAATCCAGGCGCCACCAGTTTCCGTAGTGT	350
Oy	117	ValGlnThrArgValProHisPheGlySerThrAsnSerLeuLeuTyrLeuAsnProArg	136
Db	351	GTGATGTAGCTGTGCTCCCTGGCTTTGGAGAACCTTCTCAGTGGAGTTCTCTGGACCCACC	410
Oy	137	LeuLysHisIleThrGlyTyrMetAlaProLeuAlaAspSerLeuGlnLysLeuGlyTyr	156
Db	411	AAAGACAGCGCGGTGCTCTTTTCCACACACATGCTGAGAGACCTTGTGGCGTGGGGCTAC	470
Oy	157	AlaAspGlyGlnThrLeuPheGlyAlaProTyrAspPheArgTyrGlyLeuAlaAlaGln	176
Db	471	ACAGCGGTGAGTGTGCCAGAGGGCTCCCTATGACTGGCGCGGAC-----	518
Oy	177	GlyHisProSerGlnValGlySerLysPheLeuLysAspLeuLysAsnLeuGlnGln	196
Db	519	-----CCAAATGAAACGGGGCCCTACTTCTGCTGCC---CTCGGCAGATGATCCAGAG	569
Oy	197	AlaSerAsnSerAsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyLeu	216
Db	570	ATGTACACAGCTGTATGGGGC---CCCGTGTGCTGTTGCCACAGTATGGGCAACATG	626
Oy	217	PheValIleGlnLeuLeuAsnAlaGlnProProSerTrpArgLysPheIleLysHis	236
Db	627	TACACGCTTACTTTCTGTCAGACGGCAGCCAGCCGCTGGAGACAGATATATCCGGGCC	686
Oy	237	PheIleAlaLeuSerAlaProTyrGlyGlyAlaIleAspIleMetTyrThrPheAlaSer	256
Db	687	TTCTGTGTCACATGGGTGGCGCCCTGGGGGGGGTGGCAAGACCCTGGCGCTCCGTGGTTCA	746
Oy	257	GlyAsnThrLeuGlyValIProLeuValaAspProLeuLeuValaArgAspGlnGlnArgSer	276
Db	747	GGAACACAAACCGGATCCCAAGTCATCGGGGCCCTCAAGATCCGGGAGCAGCAGCGGTCA	806
Oy	277	SerGluSerAsnLeuTrpLeuLeuProAsnProLysIlePheGlyProGlnLysProIle	296
Db	807	GCCTGTCCACAGCTGGCTGCTGCCCTACAACTAACATGATGCTACCTAGAAAGGTTC	866
Oy	297	ValIleThrProIleArgProTyrSerAlaHisAspMetValAspPheLysAspIle	316
Db	867	GTGCAGACACCCCAACATCAACTACACACTGCCGAGTACCGGAAGTCTTCCAGAGATTC	926
Oy	317	GlyPheProGlnGly---ValTyrProTyrGlnThrArgIleLeuProLeuIleGlnLysN	335
Db	927	GGCTTTAAATAGTGGCTGGCTCATGCGGACGACACAGAA-----GGGCTGGTGAAGCC	980
Oy	336	IleLysAlaProGlnValProIleThrCysIleMetGlyThrGlyValGlyLeuThrGln	355
Db	981	ACGATCCACACTGGCGGACGTGCACATGCTCTAGTAAGTGGCGTCCACACACAGAC	1040
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Search completed: February 15, 2003, 14:11:25
Job time : 232 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 15, 2003, 14:06:02 ; Search time 50 Seconds
(Without alignments)
2717.156 Million cell updates/sec

Title: US-09-857-612a-14
Perfect score: 2333
Sequence: 1 MKKEDEGKIEVATLVTVY.....GEITSINSHAEGLSNLFSG 443

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued_Patents_NA.*
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- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	100.5	4.3	1533	1	US-08-483-232-23	Sequence 23, Appl
2	100.5	4.3	1533	2	US-08-485-938A-23	Sequence 23, Appl
3	100.5	4.3	1533	2	US-08-910-041-23	Sequence 23, Appl
4	100.5	4.3	1533	3	US-09-328-474-23	Sequence 23, Appl
5	100.5	4.3	1533	3	US-09-100-546-23	Sequence 23, Appl
6	100.5	4.3	1533	3	US-09-010-715-23	Sequence 23, Appl
7	100.5	4.3	1533	4	US-09-577-758-23	Sequence 23, Appl
8	99.5	4.3	4776	2	US-08-852-401-1	Sequence 1, Appl1
9	98.5	4.2	2909	4	US-08-104-158-1	Sequence 1, Appl1
10	97.5	4.2	1041	2	US-08-602-359A-24	Sequence 2, Appl1
11	97	4.2	3048	2	US-08-313-200-2	Sequence 2, Appl1
12	97	4.2	3048	5	PCT-US93-03837-2	Sequence 2, Appl1

13	96	4.1	9510	4	US-09-453-702B-256	Sequence 256, App
14	94	4.0	1983	4	US-09-134-001C-513	Sequence 513, App
15	92.5	4.0	3128	3	US-08-716-449-1	Sequence 1, Appl1
16	92	3.9	2191	1	US-08-318-905-22	Sequence 22, Appl
17	92	3.9	2191	1	US-08-483-232-22	Sequence 22, Appl
18	92	3.9	2191	1	US-08-483-140-22	Sequence 22, Appl
19	92	3.9	2191	2	US-08-485-938A-22	Sequence 22, Appl
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23	92	3.9	2191	3	US-09-010-715-22	Sequence 22, Appl
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40	87.5	3.8	1662	4	US-08-943-714-1	Sequence 1, Appl1
41	87	3.7	1503	4	US-09-111-730-3	Sequence 3, Appl1
42	87	3.7	1875	4	US-09-877-730-23	Sequence 23, Appl
43	86	3.7	2469	4	US-09-111-730-5	Sequence 5, Appl1
44	86	3.7	1458	5	PCT-US94-03437-1	Sequence 1, Appl1
45	86	3.7	1839	1	US-08-272-875-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
Sequence 23, Application US/08483232
Patent No. 5656431
GENERAL INFORMATION:
APPLICANT: Eberhardt, Christine S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,232
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993

ATTORNEY/AGENT INFORMATION:
 NAME: No. 565643land, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/32689
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3658
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1533 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 62..1394
 US-08-483-232-23

Alignment Scores:
 Pred. No.: 0.0716 Length: 1533
 Score: 100.50 Matches: 108
 Percent Similarity: 33.52% Conservatave: 69
 Best Local Similarity: 20.45% Mismatches: 153
 Query Match: 4.31% Indels: 198
 Db: 1 Gaps: 26

US-09-857-612a-14 (1-443) x US-08-483-232-23 (1-1533)

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DB      97 CTGCACCTCCCTTGCACCTGTTATTCCTTTGACCTGGCAAGACCTGAATCCAGTCCCTA 156
QY      41 uIleProGlyAsnGlyGly--AsnGlnLeuGluAlaArgLeuThrAsnGlnTyrAsp 60
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QY      112 eAsnThrProGlyValGluThrArgVal-----Pr 122
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QY      122 oHis-----PheGlySerThrAsnSerLeuLeuLeu 132
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RESULT 2
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 ; Sequence 23, Application US/08485938A
 ; Patent No. 5847088
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.

```

? APPLICANT: Le Trong, Hai
? APPLICANT: Tjoelker, Larry W.
? APPLICANT: Wilder, Cheryl L.
? TITLE OF INVENTION: Platelet-Activating Factor
? TITLE OF INVENTION: Acetylhydrolase
? NUMBER OF SEQUENCES: 36
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
? STREET: 6300 Sears Tower, 233 South Wacker Drive
? City: Chicago
? STATE: Illinois
? COUNTRY: United States of America
? ZIP: 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/485,938A
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/318,905
? FILING DATE: 06-OCT-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/133,803
? FILING DATE: 06-OCT-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: No. 584708band, Greta E.
? REGISTRATION NUMBER: 35,302
? REFERENCE/DOCKET NUMBER: 27866/32792
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312)474-6300
? TELEFAX: (312)474-0448
? TELEX: 25-3658
? INFORMATION FOR SEQ ID NO: 23:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1533 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 62..1394
? US-08-485-938A-23

Alignment Scores:
? Pred. No.: 0.0716 Length: 1533
? Score: 100.50 Matches: 108
? Percent Similarity: 33.52% Conservative: 69
? Best Local Similarity: 20.45% Mismatches: 153
? Query Match: 4.31% Indels: 198
? DB: 2 Gaps: 26

US-09-857-612A-14 (1-443) x US-08-485-938A-23 (1-1533)
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? 340 CGACACCTTGTGATCCCAACAAAGATATTTTGGCTCTAGTAATTTCTTGAAC 399
? 122 oHis-----PheGlySerThrAsnSerLeuLeu 132
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? 132 rLeuAsnProArgLeuLysHisIleThrGlyTyrMetAlaProLeuValAspSerLeuG 152
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? 242 a-----ProTrpGlyGlyAlaIleAspGluMetTyrThrPheAlaSerGlyAsnTh 259
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? 279 rAsnLeuTrpLeuLeuProAsnProLysIlePheGlyProGlnLysProIleValIle 299
? 1042 TAAT-----ATCATTAAGATGAATAAAGCTCTTCTTACCTGATGGA----- 1081
? 299 rProIleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIleGlyPhe 319
? 1081 ----- 1081
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RESULT 3
US-08-910-041-23
Sequence 23, Application US/08910041
Patent No. 5977308
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tholker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,041
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1533 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 62..1394
US-08-910-041-23
Alignment Scores:
Pred. No.: 0.0716 Length: 1533
Score: 100.50 Matches: 108
Percent Similarity: 33.52% Conservative: 69
Best Local Similarity: 20.45% Mismatches: 153
Query Match: 4.31% Indels: 198
Gaps: 26
US-09-857-612A-14 (1-443) x US-08-910-041-23 (1-1533)
QY 9 LeuLysIleGluValAlaIleThrLeuThrValThrValValVal-MetLeuSerLeu 28
Db 37 CTGAAGCGCAGCTCAGCTTCGAGATGTTACCGTCAATTCATGCGCTTTCTGCT 96
QY 28 uCysThrCysGlyAla-----SerAsnLeuAspProLeuIle 41
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QY 41 uIleProGlyAsnGlyGly--AsnGluLeuGluAlaArgLeuThrAsnGlnTyTrLysPr 60
Db 157 TATTGAATCACCAGCATGGTGAGTAAATACAGCTCTGATGGCT----- 202
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QY 80 g-----LeuTrpPheAspSerSerValIleLeuAlaProPheThrGlnCy 95
Db 253 CGTCGGTTACAGACTTATGTTGAT----- 280
QY 95 sPheAlaGluArgMetThr-----LeuHisTyHisGlnGluLeuAspAspTyTrp 112
Db 281 -TACACTAATAAGGCGACCTCTTGCGTTGTATATCATCATCAAGATGATGATCAGC 339
QY 112 eAsnThrProGlyValGluThrArgVal-----Pr 122
Db 340 CGACACCCCTTGGATCCCAAGAAATATTTTGGCTTAAATTTCTTGAAC 399
QY 122 oHis-----PheGlySerThrAsnSerLeuLeuTy 132
Db 400 ACACAGCTGCTTGGGCAAAATATGAGCTTATTCGTTCAATGACACACTCTGCAC 459
QY 132 rLeuAsnProArgLeuLysHisIleThrGlyTyMetAlaProLeuValAspSerLeuG 152
Db 460 CTGAATGCACATCTGAGG-----ACTGGGAAAAAATACCACTAATATTTTTCGA 513
QY 152 nLysLeuGly----- 155
Db 514 TGGCTCTTGAGCATTCAGACAGATTTATTCCTATTCGATTCGCGATCCACGG 573
QY 156 -----TyrAlaAspGlyGluThrLeuPheGlyAlaProTyrAs 168
Db 574 GTTTATAGTTCGCTGCTGTAAGAACACAGGATGCTCTGCA-----TCTCGACACTACTA 627
QY 168 pPheArgTyArgLeuAlaIleGluGlyHisIleProSerGlnValGlySerLys----- 185
Db 628 TTTCAAGGACGCTGCTGCTAGAA-----ATAGCAACAAGCTCTGGCT 672
QY 186 -PheLeuLysAspLeuLysAsnLeuIleGluGluAlaSerAsnSerAsn----- 201
Db 673 CTATCTCAGAACCTTGAGCGGAGAGAGAGAGAGAGTTCCTTACCAAAATGACACTTACG 732
QY 202 -----AsnGlyLys 204
Db 733 GCACGAGCAAAAGATTTCTCAAGCTCTCAGTTGATTCTGGACATTGATGATCAGGAG 792
QY 204 sProval----- 206

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Db 793 GCCAGTGCAGAAAGTACTAGATTATTAGAGTTTGTGCGAAGACAGCTGAAGACTATTATTA 852
Qy 207 -----ILEuleuSerHisSerLeuGlyGlyLeuPheValLeuGlnLeuLe 222
Db 853 TAGGAGTAATAATAGACCATTATTGTGACATCTCTTTGGTGAGGACACAGATTATTCACACT 912
Qy 222 uasArGAsnProProSerTrpArgLysLysPheLeuLysSHisPheLeuLeuSerAl 242
Db 913 TAGTGAAGAC-----CAGAGATTTC--AGGTGGCATTTGCTTGATGC 954
Qy 242 a-----ProTrpGlyGlyAlaLeuLeuLeuLysGlyMetGlyTrpPheAlaSerGlyAsnTh 259
Db 955 ATGAGATGTTCCCGTGGCT-----GATGAGATATAT-----TTCAG 990
Qy 259 rLeuGlyValProLeuValAspProLeuLeuValAlaGAspGluGlnAlaArgSerGluSe 279
Db 991 AATTCCTCAACCCCTC-----TTTTTTATCACTCGGACAGCATTCACATCCCTTC 104H
Qy 279 rAsnLeuTrpLeuLeuProAsnProLysHisPheGlyProGlnLysProIleValIleTh 299
Db 1042 TAAI-----ATCTAAGAAATGAAAAATGCTTCTTACTGATAGA----- 1081
Qy 299 rProIleArgProTrpTyrSerAlaHisAspMetValAspPheLeuLysAspIleGlyPhePr 319
Db 1081 ----- 1081
Qy 319 oGluGlyValAlaTyProTyrGluThrArgIleLeuProLeuIleGlyAsnIleLysAlaPr 339
Db 1082 -----GAGCGAAAAATGATTACCAATCAGGAGGTGGTCCATCAGAA 1122
Qy 339 oGlnValProIleThrCysIleMetGlyThrGlyValGlyThrLeuGluThrLeuPheTy 359
Db 1123 TTTTGTTGACTCAGCTTTTCCACATGACCAAAATAAATGGCTACATATTCACACTG----- 1177
Qy 359 rGlyLysGlyAspPheAspGlnArgProGluIleSerTyrGlyAspGlyAspGlyThrVa 379
Db 1178 ----AAAGAGACACTTCGATTCCAATGATAGCATCAGCCTTACCAACAAAAGTTCCTTAGC 1233
Qy 379 lAsnLeuValSerLeuLeuAlaLeuGln-----SerLeuTrpIly 392
Db 1234 GTTCTTCACAAAACATTTTAGCACTTCAGAAAGATTTTGTAGTCAGTGGGATTCCTTAGTTGA 1293
Qy 392 sGluGluLysAsnGlnTyrLeuLysValValLysHisAspGlyValSerHisThrSerI 412
Db 1294 AGGGGAAGATCACAAATCTTATTTCCAGGAGCAACAATTAACAACACCAACCAAGCAT 1355
Qy 412 eLeuLysAspGluValAlaLeu 419
Db 1354 TCTCGAACAATCCACAGAGATA 1375

RESULT 4
US-09-328-474-23
: Sequence 23, Application US/09328474
: Patent NO. 6045794
: GENERAL INFORMATION:
: APPLICANT: Cousens, Lawrence S.
: APPLICANT: Eberhardt, Christine D.
: APPLICANT: Gray, Patrick W.
: APPLICANT: Le Trong, Hai
: APPLICANT: Tjoelker, Larry W.
: APPLICANT: Wilder, Cheryl L.
: TITLE OF INVENTION: Platelet-Activating Factor
: TITLE OF INVENTION: Acetylhydrolase
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bornun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
:

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1      MEDUM TYPE: Floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: PatentIn Release #1.0, Version #1.25
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/09/328,474
7      FILING DATE:
8      CLASSIFICATION:
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: US 08/483,232
11     FILING DATE: 07-JUN-1995
12     PRIOR APPLICATION DATA:
13     APPLICATION NUMBER: US 08/318,905
14     FILING DATE: 06-OCT-1994
15     PRIOR APPLICATION DATA:
16     APPLICATION NUMBER: US 08/133,803
17     FILING DATE: 06-OCT-1993
18     ATTORNEY/AGENT INFORMATION:
19     NAME: Rin-Laures, Li-Hsien
20     REGISTRATION NUMBER: 33,547
21     REFERENCE/DOCKET NUMBER: 27866/34026
22     TELECOMMUNICATION INFORMATION:
23     TELEPHONE: (312) 474-6300
24     TELEFAX: (312) 474-0448
25     TELEX: 25-3658
26     INFORMATION FOR SEQ ID NO: 23:
27     SEQUENCE CHARACTERISTICS:
28     LENGTH: 1533 base pairs
29     TYPE: nucleic acid
30     STRANDEDNESS: single
31     TOPOLOGY: linear
32     MOLECULE TYPE: protein
33     FEATURE:
34     NAME/KEY: CDS
35     LOCATION: 62..1394
36     US-09-328-474-23
37
38 Alignment Scores:
39 Pred. No.: 0.0716 Length: 1533
40 Score: 100.50 Matches: 108
41 Percent Similarity: 33.52% Conservative: 69
42 Best Local Similarity: 20.45% Mismatches: 153
43 Query Match: 4.31% Indels: 198
44 DB: 3 Gaps: 26
45
46 US-09-857-612A-14 (1-443) x US-09-328-474-23 (1-1533)
47
48 QY 9 LeuyslllegluValAlaThleuthValylValVal -WleuSerLeuLe 28
49      ||||| ::::::::::| ||||| |||
50 Db 37 CTGAACAGCGACGCTCAGCTCGAGATGTACCGTCCAAATGCGCTTTGTCGCT 96
51
52 QY 28 ucysrhrcysgluAla-----SerAsnLeuAspProleuLele 41
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54 Db 97 CTGCACGCGCTTCGACGCTGTTATCTTTGACGCGACAGACCTGAATCCAGTTGCTA 156
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56 QY 41 uileProgluAsnlglyl--AsnGlnLeuAlaAlaArgleuthrAsnGlnTyLysPr 60
57      ||| ::::::::::| |||
58 Db 157 TATTGAATACACAGCATGGCGATGACATGAAGATCAAGCTCTGATGCT----- 202
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60 QY 60 oSerThrPheIleCysGluSerTrrTyProleuIleLysLysLysAsnGlyTrrPheAr 80
61      ::| ||| ::::||| |||
62 Db 203 -GCTGCACAAACATGTGTCATCTAAATACCC-----AGAGGAATATGATCTTTATTC 252
63
64 QY 80 g-----LeuTrpPheAspSerValIleleuAlaProPheThrGlnCy 95
65      ||| |||||
66 Db 253 CGTCGCTTGACAGCATGATGATTTGAT----- 280
67
68 QY 95 sPheAlaGluArgMetThr-----LeuIleTyGlnIleGlnIleuAspAspTyrrh 112
69      ::| ::| ||| ||::||| ::| |||||::
70 Db 281 -TACACGTATTAAGGACACCTCTTGCGCTTTGTATTATTCATGCAATGATATGATCAGTC 339
71
72 QY 112 eAsnThrProgluValAlaGluThrArgVal-----Pr 1222
73      ::||| | ::|

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APPLICATION NUMBER: US 08/133,803
 FILING DATE: 06-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 6146625and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/32793
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-0448
 TELEFAX: 25-3658
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1533 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 62..1394
 US-09-010-715-23

Alignment Scores:
 Pred. No.: 0.0716 Length: 1533
 Score: 100.50 Matches: 108
 Percent Similarity: 33.52% Conservative: 69
 Best Local Similarity: 20.45% Mismatches: 153
 Query Match: 4.31% Indels: 198
 DB: Gaps: 26

US-09-857-612a-14 (1-443) x US-09-010-715-23 (1-1533)

QY 9 LeuLysIleGluValAlaThrLeuThrValThrValValVal-MetLeuSerLeu 28
 DB 37 CTGAAACGGCAGCTGCTCGAGATGTTACCGTCAATATGCAGCGCTTTTCGCT 96
 QY 28 uCysThrCysGlyAla-----SerAsnLeuAspProLeuIleLe 41
 DB 97 CTGCAACCTGCTTGCATGCTTTATCCTTTGACTGCAAGACCTGAATCCAGTGCCTA 156
 QY 41 uIleProGlyAsnGlyGly--AsnGlnLeuGlnAlaArgLeuThrAsnGlnTyrSer 60
 DB 157 TATTGAATCACCAACGATGGGTGATGATGACAGCTCTGATGGCT----- 202
 QY 60 oSerThrPheIleCysGlnSerTyrPyrProLeuIleLysLysAsnGlyTyrPheAr 80
 DB 203 -CCTGCAACATTTGGTCATCTAAATCC-----AGAGAAATGATGATCTTATTC 252
 QY 80 g-----LeuTyrPheAspSerSerValIleLeuAlaIleProPheThrGlnC 95
 DB 253 CCGTGGTGTACAGACTTCGATGTTGAT----- 280
 QY 95 sPheAlaGluArgMetThr-----LeuHisTyrHisGlnGluLeuAspSerPyr 112
 DB 281 -TACACTAATAGGCGACCTTCTGCGTTGATATTCATCTCAAGATGATGATCAGTC 339
 QY 112 eAsnThrProGlyValGluThrArgVal-----Pr 122
 DB 340 CGACACCCCTTGGATCCCAACAAGAAATTTTGGCTTAGTAATTTCTTGGAAC 399
 QY 122 oHis-----PheGlySerThrAsnSerLeuLeu 132
 DB 400 ACATCGGCTTGTGGCAAAATATATGCGCTTATCTCGGTCAATGACAACTCCGACG 459
 QY 132 rLeuAsnProArgLeuLysHisIleThrGlyTyrMetAlaProLeuValAspSerLeu 152
 DB 460 CTGGAATGCACATCTGAG-----ACTGGGAAAAAATACCCACTAATATTTTTCCTCA 513
 QY 152 nLysLeuGly----- 155
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 QY 156 -----TyrAlaAspGlyGluThrLeuPheGlyAlaProTyrAs 168

DB 574 GTTATAGTTCGCTGTAGAACACAGCGATGGCTCTGCA-----TCCGACATACCTA 627
 QY 168 pPheArgTyrGlyLeuAlaAlaGluLysProSerGlnValGlySerLys----- 185
 DB 628 TTTCAGGACCACTCTGCTGTAGA-----ATAGGCAACAAGCTTGGCT 672
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 DB 673 CTATCTCAGAACCCCTGACAGAGAGAGAGGTTTCTTACGAATAGACAGCTTAGG 732
 QY 202 -----AsnGly 204
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 QY 204 sProVal----- 206
 DB 793 GCCAGTGACCAATGTACTGATTTAGAGTTTGATGTGGAAACAGCTGACGACTCTATTGA 852
 QY 207 -----IleLeuLeuSerHisSerLeuGlnGlyLeuPheValLeuGlnLeu 222
 DB 853 TAGGATAAATAGCCATTATTTGACATCTTTGGTGGAGCAGCTTATTCAGACTCT 912
 QY 222 uAsnArgAsnProProSerTyrPheGlyLysPheIleLysHisPheIleAlaLeuSerAl 242
 DB 913 TAGTGAGAC-----CAGAGATTC--AGGTGCGCATGCTCTGATGC 954
 QY 242 a-----ProTyrPylGlyAlaIleLeuAspGluMetTyrThrPheAlaSerGlyAsn 259
 DB 955 ATGGATGTTTCCCGTGGT-----CATGAGATAT-----TCCAG 990
 QY 259 rLeuGlyValProLeuValAspProLeuLeuValArgAspGlnArgSerSerLeu 279
 DB 991 AATTCCTCAACCCCTC-----TTTTTATCAACCTGGAACAGATTCCATACCCCTTC 1041
 QY 279 rAsnLeuThrLeuLeuProAsnProLysIlePheGlyProGlnLysProIleValIle 299
 DB 1042 TAAT-----ATCATAGAAATGAAAAAATGCTTCTTACTGATGAGA----- 1081
 QY 299 rProIleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIleGlyPhe 319
 DB 1081 ----- 1081
 QY 319 oGlnGlyValTyrProTyrGluThrArgIleLeuProLeuIleGlyAsnIleLysAla 339
 DB 1082 -----GAACGAAATATGATTAACAATCAGGGGTGCGTCATCAGAA 1122
 QY 339 oGlnValProIleThrCysIleMetGlyThrGlyValGlyThrLeuGluThrLeuPhe 359
 DB 1123 TTTTGTGACTTCACCTTTTGGCAGTAAATATTTGGCTACCTATTCACACTG----- 1177
 QY 359 rGlyLysGlyAspPheAspGluArgProGluIleSerTyrGlyAspGlyAspGlyThr 379
 DB 1178 -----AAAGGACACATGATTCATCAATGATGACCATTCAGCAACAAAGCTCTTAC 1233
 QY 379 lAsnLeuValSerLeuLeuAlaLeuGln-----SerLeuTyr 392
 DB 1234 GTTCTTACAAAAAATTTAGACCTTCAGAAAGATTTTGATCGTGGAGATTCTTAGTTGA 1293
 QY 392 sGlnGluLysAsnGlnTyrLeuLysValValLysIleAspGlyValSerHisThrSer 412
 DB 1294 AGCGAAGATCAACAATCTTATTCAGAGCAACAATTTAAACAACACCAACAGCCAT 1353
 QY 412 eLeuLysAspGluValAlaLeu 419
 DB 1354 TCTGGAACCTCCACAGAAATA 1375

RESULT 7

US-09-577-758-23
 Sequence 23, Application US/09577758
 Patent No. 6203790

GENERAL INFORMATION:
 APPLICANT: Cousens, Lawrence S.

```

1  APPLICANT:  Eberhardt, Christine D.
2  APPLICANT:  Gray, Patrick W.
3  APPLICANT:  Le Trong, Hai
4  APPLICANT:  Tjoelker, Larry W.
5  APPLICANT:  Wilder, Cheryl L.
6  TITLE OF INVENTION:  Platelet-Activating Factor
7  TITLE OF INVENTION:  Acetylhydrolase
8  NUMBER OF SEQUENCES:  30
9  ADDRESSSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
10 STREET:  6300 Sears Tower, 233 South Wacker Drive
11 City:  Chicago
12 STATE:  Illinois
13 COUNTRY:  United States of America
14 ZIP:  60606-6402
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE:  Floppy disk
17 COMPUTER:  IBM PC compatible
18 OPERATING SYSTEM:  PC-DOS/MS-DOS
19 SOFTWARE:  Patentln Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER:  US/09/577,758
22 FILING DATE:
23 CLASSIFICATION:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:  09/010,715
26 FILING DATE:
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER:  US 08/133,803
29 FILING DATE:  06-OCT-1993
30 ATTORNEY/AGENT INFORMATION:
31 NAME:  No. 6203790and, Greta E.
32 REGISTRATION NUMBER:  35,302
33 REFERENCE/DOCKET NUMBER:  27866/32793
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE:  (312) 474-6300
36 TELEFAX:  (312) 474-0448
37 TELEX:  25-3658
38 INFORMATION FOR SEQ ID NO:  23:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH:  1533 base pairs
41 TYPE:  nucleic acid
42 STRANDEDNESS:  single
43 TOPOLOGY:  linear
44 MOLECULE TYPE:  protein
45 FEATURE:
46 NAME/KEY:  CDS
47 LOCATION:  62..1394
48 US-09-577-758-23
49
50 Alignment Scores:
51 Pred. No.:  0.0716  Length:  1533
52 Score:  100.50  Matches:  108
53 Percent Similarity:  33.52%  Conservative:  69
54 Best Local Similarity:  20.45%  Mismatches:  153
55 Query Match:  4.31%  Indels:  198
56 Gaps:  26
57
58 US-09-857-612A-14 (1-443) x US-09-577-758-23 (1-1533)
59
60 9 LeuysIleGluValAlaIaThleuThrValAlhValValVal-MetIeuSerLeuLe 28
61 ||||| :|||:|  ||||| |||  |||  ||
62 37 CTGAAGCGGAGGCTTACGCTTGCGAGAGATCTTACCGTCCAAATTTGCATGGCGCTTTCGTGCT 96
63
64 28 uCysThrCysGlyAla-----SerAsnIeuSpsProIeuIleLe 41
65 ||||| |||  |||  :|||:| |||:|
66 97 CTCGACCTGCTTGCACTGCTTTATCTTTTGACTGGCAGACCTGATCCAGTTCGCTTA 156
67
68 41 uIlleProIySngIyGly---AsngInIleuGluAlaIargIeuThrsngInIyrlYsPr 60
69 |||  :|||:| |||  :|||:| |||:|
70 157 TATTGATATCACACAGCAGTGGCTGACATGATACAAAGCTCTGATGGCT----- 207
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72 60 oSerThrPheIleCysGluSerTrpTyrProIeuIleuysIySylsAsngIyTrpPhear 80

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Db	253	CGTGGCTTGTACACACTTGATGTTTGAAT	-----						280
Qy	95	sPheAlaIleArgMetThr-----	-----	-LeuHisTyrHisIleGlnIleLeuAspAspTyrPh					112
		..::	..::		..::		..::		..::
Db	281	-TACATTAATGAAGGACACCTTCTGCGTTGTATTAATCATCTCAACATGATGATCATCTC							339
Qy	112	eAsnThrProGlyValIleGuthrAlaVal-----	-----	-----	-----	-----	-----	-----	122
Db	340	CGACACCCCTTTGGATCCCAACAAAGAATATTTTGGGCTTAGTAATTCCTTGGAAC						-Pr	399
Qy	122	ohis-----	-----	-PheGlySerThrAsnSerIleuLeuTy					132
Db	400	ACACTGGCTTTGGGCAAAATTTATGGCGTTATCTTCTGGCTTCAATGACACATCTCCGACG				..::			459
Qy	132	rLeuAsnProArgIleuLeuHisIleThrGlyTyrMetAlaIleProLeuValAspSerLeuG1							152
Db	460	CTGGAATGCACATCTGAAG-----	-----	-ACTGGGGAAATATCCACATATTAATTTTCTCA					513
Qy	152	nLysLeuGly-----	-----	-----	-----	-----	-----	-----	155
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Qy	156	-----	-----	-TyrAlaAspGlyIleThrLeuPheGlyValIleProTyrAs					168
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Qy	168	rPheArgTyrGlyLeuAlaIleGlnGlyHisProSerGlnValGlySerLys-----	-----	-----	-----	-----	-----	-----	185
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Qy	202	-----	-----	-AsnGlyIy					204
Db	733	GCAACGACAAAGAAATGTTCTCAAGCTCCAGTTTGATTTCTGGACATTCGATCAGCGGAG				..::		..::	792
Qy	204	sProVal-----	-----	-----	-----	-----	-----	-----	206
Db	793	GCCAGTGCAGATGTAAGTATTAGAGTTGATGTGGAAACACCTGAGAGACTTATTGA							852
Qy	207	-----	-----	-IleLeuLeuSerHisSerLeuGlyIleLeuPheValLeuGlnLeuIle					222
Db	853	TAGGATATAAATTAAGCATTATTAAGCACTTCTTTGGTGGAGCAGCAAGTTATTCAGACTCT		..::			..::		912
Qy	222	uAsnArgAsnProProSerThrAlaGlyLysPheIleLysHisPheIleAlaLeuSerAl							242
Db	913	TAGTGAAMGAC-----	-----	-CAGACATTC--	..::		..::		954
Qy	242	a-----	-----	-ProThrArgIleGlyAlaIleAspGlnMetTyrThrPheAlaSerClyAsnTh					259
Db	955	ATGGATGTTTCCCGGGT-----	-----	-GATGAAGTATAT-----	..::		..::		990
Qy	259	rLeuGlyAlaIleProLeuValAspProLeuLeuValArgAspGlnArgSerSerGluSe							279
Db	991	AATTCCTCAACCCCTC-----	-----	-TTTTTATTCACACTCGGAACGATTCCAATACCCCTTC			..::		104
Qy	279	rAsnLeuTrpLeuLeuProAsnProLysIleIlePheGlyProGlnLysProIleValIleTh							299
Db	1042	TAAAT-----	-----	-ATCTATAGAAATGAAGAAATATCTTCTTACCTGATAGA-----			..::		108
Qy	299	rProIleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIleGlyPhePr							319
Db	1081	-----	-----	-----	-----	-----	-----	-----	108
Qy	319	oGlnGlyValTyrProTyrGlnThrArgIleLeuProLeuIleGlyAsnIleLysAlaPr				..::		..::	339

Db	1082	-----GACGAAAAATGATTACAACTCAGGGGTGGGTCCATCAGAA	1122
QY	339	oGlnValProlIethrCysIleMetelYhrIglYValIglYThrIleGluThrLeuPheTY	359
Db	1123	TTTTGTGTACCTCATTCTTCCACTAGCAAAATAATATGGCTGCTATTCACACTG----	1177
QY	359	rGlyLysGlyAspPheAspIuArGrProGluIleSerTYrGlyAspGlyAspGlyThrVa	379
Db	1178	-----AAGGAGACATCGATTCCAAATGATAGCACACCTTACGACAAAGAATCTCTTAGC	1233
QY	379	IAsnLeuValSerLeuLeuAlaLeuGln-----SerLeuTrpIly	392
Db	1234	GTTCTTACAAAACATTATAGCACTTCAGAAAGACATTTTGATCGAGTGGCATCTTTATGTTGA	1293
QY	392	sGluGluLysAsnGlnTYrLeuLysValValLysIleAspCylValSerHisThrSerI	412
Db	1294	AGCGGAGATCACAAATCTTATTCACAGGAGCAACATTATACACCAACCAACCAAGCCAT	1353
QY	412	eLauLysAspGluValAlaLeu	419
Db	1354	TCCTCAGAACTCCACAGAGATA	1375

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RESULT 8
US-08-852-401-1
Sequence 1, Application US/08852401
Patent No. 5976836
GENERAL INFORMATION:
APPLICANT: Weber, J. Mark
APPLICANT: Hessler, Paul E.
APPLICANT: Larsen, Peter E.
APPLICANT: Luu, B. Minh
TITLE OF INVENTION: Methods and Compositions for Enhancing
TITLE OF INVENTION: Erythromycin Production
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite
STREET: 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,401
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa L.
REGISTRATION NUMBER: 38, 978
REFERENCE/DOCKET NUMBER: FER2159PO030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4776 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-852-401-1

Alignment Scores:
Pred. No.: 0.584 Length: 4776
Score: 99.50 Matches: 77
Percent Similarity: 32.55% Conservative: 52
Best Local Similarity: 19.25% Mismatches: 131
Query Match: 4.26% Indels: 11

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Alignment Scores:	
Pred. No.:	0.584
Score:	99.50
Percent Similarity:	3.25%
Best Local Similarity:	19.25%
Query Match:	4.26%
Length:	4776
Matches:	77
Conservative:	52
Mismatches:	131
Indels:	141

DB:	2	Gaps:	16
US-09-857-612A-14 (1-443)	x	US-08-852-401-1 (1-4776)	
QY	82	TrpHeaSpSerSerValIleLeuAlaProPheThiGlycysPheAlaGluArgMetThr	101
Db	1910	TGtGGGGCGAGCGGGGGTGTACAGAGTCTACGTCCGAGCTTGGCGGAC-----	1966
QY	102	LeuHisTyrHisGlnGluLeuAspAspTyrPheAsnThrProGlyIleValGluThrArgVal	121
Db	1961	-----GCCGCGCGCGAGCGGGATCGCGAGCACTGGCGGGGTGGCGCAGAGCTG	2008
QY	122	ProHisPheGlySerThrAsn-----SerLeuLeuTyrIleAsnProArgLeuHisHisIle	140
Db	2009	CCGTAACCTGGTGGAGCTGGGTGGAGACGGGGTGTGGCTACACCGC-----	2055
QY	141	ThrGlyTyrMetAlaProLeuValAsp-----SerLeuGlnIleGluGlyTyrIleAspGly	159
Db	2054	---TTCACACCGGTGGCGGAGTGGCGAGCGGGGTACGACAGTGGCGAGTACACGACGTC	2110
QY	160	GluThrLeuPheGlyAlaProTyrAspPheArgTyrGlyLeuAlaIleGluHisPro	179
Db	2111	GAACCGATGTTCGGCAGC-----	2128
QY	180	SerIleValGlySerIysPheLeuLysAspLeuLysAsnLeuIleGluIleAsnSerIle	199
Db	2129	-----CTCGACGACTCTCGACGACCTCTGGCGGGCG-----	2161
QY	200	SerAsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyGlyLeuPheValLeu	219
Db	2162	-----CACTGCTGTGGCTGAGGTGATCTCTC	2188
QY	220	GlnLeuLeuAsnArgAsnProProSerTyrArgLysLysPheIleIysHisPheIleAla	239
Db	2189	GACGTGCTGCCCAACACACACACTCCGACGCGGACCCGCTGGTGGCGGAG-----	2239
QY	240	LeuSerIleArgProIrrpGlyAlaIleAspGluMetTyrThrPheAlaSerGly-----	257
Db	2240	CTGGAGCGCGGCGCGGCGGACCGCGCGGAGCGGTACTGTCTCCGCGACGCGGCGCGC	2299
QY	258	-----AsnThrLeuGlyValProLeuValAsp	266
Db	2300	GAGAGCGGGGAGCTGCCGCCCAACGACTGGAGATCTCTTGGGGGTCCGCC-CTGAGAC	2358
QY	267	ProLeuLeuValArgAspGluArgSerSerGluSerAsnLeuTrpLeuLeuProAsn	286
Db	2359	CCG-----	2361
QY	287	ProLysIlePheGlyProGlnLysProIleValIleThrProIleArgProTyrSerIleA	306
Db	2362	-----CGTCCCGACGCGCGAGGTACTGCACTGCCTGTTGCGCCCGACACACC	2409
QY	307	His-----Asp-MetValAspPheLeuLysAspIleGlyPhe-	318
Db	2410	CGACCTGAACCTGGCGGCAACCCGAGATTCGGCGCGAGTTCCGCAAGGTCTGGAGTTCTG	2469
QY	319	---ProGluGlyValTyrTyrProTyrGlyIleThrArgIleLeuProLeuIleGlyAsnIleLys	337
Db	2470	GCTGAGCGCGGGGTGAGAGGCTTC-----CGGATCGACGTCCGCCACGAGATGATCA	2523
QY	337	GAlaProGlnValProIleThrCysIleMetGlyThrGlyValGlyThrLeuGlnThrIle	357
Db	2524	GCAACCCGACCTCC-----GACACCGGGCGCGCACGACGATCTCCT	2568
QY	357	uPheTyrGlyLysGlyAspPheAspLysArgProGluIleSerTyrGlyAspGlyAspGly	377
Db	2569	GCTC-----GGCGGGCGAGCTGCCCTACTTTCGACAGAGACGA	2607
QY	377	YThrValAsnLeuVal-----SerLeuLe	385
Db	2608	GGTGACGCGGATCTACCGGGGAGTGGCGCGAGCTGCTGACAGTCTTACAGAGGCGCGGAT	2667
QY	385	uAlaLeuGlnSerLeuTrpLysGluGlnLysAsnGlnTyrIleLysValValLysIleAs	405

OY	377	YTHValAsnLeuVal-----	SerLeuLe	385
		:::	:::	
Db	2608	GGTGCACGGCATCTACCGGAGAGTGGCGCGAGCTGCTGCACCTCCTACGAGAGCGCGCCGGAT		2667
OY	385	uAlaLeuGlnSerLeuTrpLysCluGlnLysasnGlnTyrLeuLysValValLysIleAs		405

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Db 2668 CGGGGTGCGGAGCGTGGGCGCCGACCAAGTCAAGCGCTGGCCGCTACGTGGCCGCGA 2727
QY 405 pglYvalSerHisThr----- 410
Db 2728 CGAGCTGCACCGAGCGTTCAACATGCGGCTCTTGAGTCCGCCGTGTCGCCGACGCGTT 2787
QY 411 -----SerIleuLysAspGluValAlaLeuAsnGluIleValGlyGluIleThrSer 428
Db 2788 CCGCGCGGTATGACGACATCGCTCGCGGCCACAGCCCGCTCGGGGCGACACGACC 2845

RESULT 9
US-08-104-158-1
Sequence 1, Application US/08104158
Patent No. 6215042
GENERAL INFORMATION:
APPLICANT: Wilmitzer, Lothar
APPLICANT: Sonnewald, Uwe
APPLICANT: Kossmann, Jens
APPLICANT: Mueller-Roeber, Bernd
APPLICANT: Visser, Richard Gerardus Franciscus
APPLICANT: Jacobsen, Evert
TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostroienk, Faber, Gerb & Sofien
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,158
FILING DATE: 13-AUG-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP PCT/EP92/00302
FILING DATE: 11-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 41 04 782.6
FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: FA-1996 PCT (951-91)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-382-0700
TELEFAX: 212-382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2909 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum cv. Desiree
STRAIN: Desiree
DEVELOPMENTAL STAGE: growing tuber
TISSUE TYPE: tuber
CELL TYPE: total tuber
IMMEDIATE SOURCE:

```

```

; LIBRARY: cDNA of total tuber mRNA in pUC 19 (hinc II)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..1699
; OTHER INFORMATION: /note= "for Branching enzyme I
; OTHER INFORMATION: (partial) truncated protein; 97,11 % identity to
; OTHER INFORMATION: active potato branching enzyme"
US-08-104-158-1

Alignment Scores:
Pred. No.: 0.344 Length: 2909
Score: 98.50 Matches: 93
Percent Similarity: 32.91% Conservative: 63
Best Local Similarity: 19.62% Mismatches: 151
Query Match: 4.22% Indels: 167
DB: 4 Gaps: 25

US-09-857-612A-14 (1-443) x US-08-104-158-1 (1-2909)
QY 32 GLVALASerAsnLeuAspProLeuIleLeuIleProGlyAsnGlyAsnGluLeu 51
Db 152 GGCCTCCCTAAATTGGATCCA-----ACTTTGGAA 181
QY 52 AlaArgLeuThrAsn-----GlnTyrLysProSerThrPheIleCys 65
Db 182 CCTATCTAGATCACTTCAGACACAGAAATGAAGATATGTGATCAGAAATGCTCAT 241
QY 66 GluSerTyrPyr---ProLeuIleLysLysAsnGlyTTPheArgLeuTrpPhe--- 83
Db 242 GAAAAATATGAGGCGACCCCTTGAGGAATTCCTCAAGGTATTTAAATTTGGATTCAC 301
QY 84 -----AspSerSerValIleLeu-----AlaProPheThrGln----- 94
Db 302 AGGCAAGATGCTGATGATGCTATGCTGAATGGCTCTCTGCTCCACAGAAACCAACT 361
QY 95 -----CysPheAlaGluArgMetThrLeuHisTyrHisGlnGluLeuAspPyr--- 111
Db 362 ATTGCGCATTTCAATGATGAGAGAGCGTTCTAACCAATGATGAGAAAGACAGATTGGT 421
QY 112 -----PheAsnThrProGlyValGluThrArg-----ValProHisPheGlySer 126
Db 422 GTTGGAGTATTAGAAATTCCTGATGTGACAGTAGACGATCCACAC----- 472
QY 127 ThrAsnSerLeuLeuTyrLeuAsnProArgLeuLysHisIleThrGlyTyrMetAlaPro 146
Db 473 ---AACTCCAGAGTTAACTT---CGTTTCACACATGCTAATGAGTGTGGTAACT 523
QY 147 LeuValAspSerLeuGlnLysLeuGlyTyrAlaAspGlyGluThrLeuPheGlyAlaPro 166
Db 524 CGTATCCCTGCTGTGATTAAGATGATGCCACGACAGCGCC---ACAAAGTTTGCACACCA 580
QY 167 TyrAsp-----PheArgTyrGlyLeu 173
Db 581 TATGATGTGTCTACTGGACCCACCACTTCAGAAAGTACCACTCAATATACCTCGC 640
QY 174 AlaAla-----GluGlnHisProSerGlnValGlySer--- 184
Db 641 CCTCCCAACCCCGACGCCCAAGATCTACGAAAGACATGTCGGCATAGACAGCTCTAG 700
QY 185 -----LysPheLeuLysAspLeuLysAsnLeuIleGluGluAla 197
Db 701 CCAGCTGTAATTCGTATCGTATCGAGTGTGCAGATGATGTTTAACTCCGATTT---AAGCA 757
QY 198 SerAsnSerAsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyGlyLeuPhe 217
Db 758 AATAACTATTAATCTGCTCAGTGTGCGCATTAAGGAACATTTCTTACTATGAGTCAATT 817
QY 218 ValLeuGlnLeuLeuAsnArgAsnProProSerTrpArgLysLysPheIleLysHisPhe 237
Db 818 GGATATCATGTTACAAAC-----TTT 838
QY 238 IleAlaLeuSerAlaProTyrGlyGlyAlaIleAspGluMetTyrThrPheAlaSerGly 257

```



```

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,200
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-20658, 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3048 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Mature
TISSUE TYPE: Thyroid gland(from patients with Grave's
TISSUE TYPE: disease)
IMMEDIATE SOURCE:
CLONE: phppo-2.8
POSITION IN GENOME:
MAP POSITION: 2pter-q11
FEATURE:
NAME/KEY: CDS
LOCATION: 73..2871
PUBLICATION INFORMATION:
AUTHORS: Kimura, S.
AUTHORS: Kotani, T.
AUTHORS: McBride, O.W.
AUTHORS: Umeki, K.
AUTHORS: Nakayama, T.
AUTHORS: Ohlaki, S.
AUTHORS: Hirai, K.
TITLE: Human Thyroid peroxidase: Complete cDNA and
TITLE: protein sequence, chromosome mapping, and
TITLE: identification of two alternately spliced mRNAs
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 84
PAGES: 5555-5559
DATE: 1987

US-08-313-200-2
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 3048

Alignment Scores:
Pred. No.: 0.557 Length: 3048
Score: 97.00 Matches: 98
Percent Similarity: 33.78% Conservative: 52
Best Local Similarity: 22.07% Mismatches: 146
Query Match: 4.16% Indels: 149
DB: 2 Gaps: 24

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Oy	84	AspSerSerValIleLeuAlaProPheThrInGlySerPheAlaGluArgMetThrLeuIis	103
Db	393	GAATCACTCAACATCACACGATCC---AACGGATGTTTATGAGAAGATCTGCGAGCAT	449
Oy	104	TYR-----HisGlnGluLeuAspAspTyrPheAsnThr	114
Db	450	CATTGCAAACTGTCGTGATGTCCTCCCTTACATGAGCTGCCCAAAATAGCCAAACACTTG	509
Oy	115	ProGlyValGluThrArgValIProHisPheGlySerThrAsnSerLeuLeuTyrLeuAsn	134
Db	510	CCTGGCAGAACAAATACAGGGCCATCAC-----AGGAGCTTCCACACACAGAGA	557
Oy	135	Pro-----ArgLeuLysHisIleThrGlyTyrMetAlaProLeu-ValAspSe	150
Db	558	CCACCCACGATGGGGCGCCCTCCCAACAGGGCCCTGGACGATGCTCCTCCAGTC-----	612
Oy	150	rLeuGlnLysLeuGlyTyrAlaAspGlyGluThrLeuPheGlyAlaProTyrAspPheAr	170
Db	613	-----TATAGAGACGGC-----TTCAGCTCAGCCCGGAGGCTTGGA	647
Oy	170	gTyrGlyLeuAlaAlaGluGlyHisProSerGlnValGlySerLysPheLeuLysAspLe	190
Db	648	CCCCGGCTTCTTGACACAGCGGTTCCTCACTGCCCGCGCGGAGGTCACAGACATGT	707
Oy	190	uLysAsnLeuIleGlnGluLysAsnSerAsnAsnGlyLysProValIleLeuLeuSe	210
Db	708	CATTCAAGTTTCAATATGAGTGTGTCACAGATGATGACCGCTATCTGACCTTCGTATG--	765
Oy	210	rHisSerLeuGlyGlyLeuPheValLeuGlnLeuLeuAsnArgAsnProProSerTrrAr	230
Db	766	-----GCATGG-----	771
Oy	230	gLyLysPheIleLysHisPheIleAlaLeuSer-----AlaProTyr	244
Db	772	-GGACATACATGACACGACATCCGCTTACACACACACAGACACACGAAAGATCGCTT	830
Oy	244	pglyGlyAlaIleAspGluMetTyrThrPheAlaSerGlyAsnThrLeuGlyValProLe	264
Db	831	CGGGGGGGGGCTGACACGCCAGATGACTTGTGAACCAACAAACCA-----	876
Oy	264	uValAsProLeuLeuValArgAspGlnGlnArgSerSerGlnSerAsn-----LeuTr	282
Db	877	-TGTTTCCCATACACTCCCGGAGAGACCGCGCGCGGGCACCAGCTGTCTGTCC	935
Oy	282	pLeuLeuProAsnProLysIlePhe-----GlyProGlnLysProI	296
Db	936	-CTTCTACCG-----CTCTTGGCGCGCTCGCGGACCGGAGCCAAAGCGCGCTCT	985
Oy	296	eValIleThrProIle-----ArgProTyrSerAlaHisAspMetValAspPheLeuLy	314
Db	986	T---TGGAACTGTCCACGCGCAACCGCGGCGAGCATGAAAGGATGACCTGTCTCC	1042
Oy	314	sAspIleGly-----	317
Db	1043	TGGACGGGTCCACCGCTATGGAAGCGTCCCGGCCCTTACAGAGCAAGCTCGGAAACTGGA	1102
Oy	318	--PheProGlyGlyValTyrTyrProTyrGluThrArgIle-----L	330
Db	1103	CCAGTGGCCGAAGGGCTCTCCGCGTCCACGCGCGCTCCGGGACTCCGCGCGCCCTAC	1162
Oy	330	eupProLeuIleGlyAsnIleLysAlaProGlnValProIleThrCysIleMetGlyThrG	350
Db	1163	TGCGCTTCGTG-----CCGCGACAGGGGCGCTCGGCGCTGTGCGCCCGAGCCG	1210
Oy	350	lyValGlyThrLeuGluThrLeuPheTyrGlyLysGlyAspPheAspGluArgProGluI	370
Db	1211	GCATC-----CCCGAG	1222
Oy	370	leSerTyrGlyAsp-----GlyAspGlyThrValAsnLeuVal---SerLeuL	385
Db	1223	AGACCCGCGGGCGCTGCTCTGTGCGCGAGACGGCGCGCCACAGCAGATGCTCCCTCGGA	1282

QY 385 euAlaLeuGlnSerLeuTrpLysGluGluLysAsnGln----- 397
| | | | | : : : : : | | | : : : : :
Db 1283 CGGACTGACACGCTGTGCTCGCGAGCACACCGCTGCGCGCGCTCAAGGCC 1342
QY 398 -----TyrLeuLysValValLysIleAspGlyValS 408
| | | | | : : : : : | | | : : : : :
Db 1343 TCATGCGCAGCTGAGCGCGAGCCGCTGTACCAAGAGCGCGCAGGTGTGCGGCTC 1402
QY 408 erHisThrSerIle-----LeuLysAspGluVal-----AlaLeuA 420
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Db 1403 TGCACGATCATCACCCTGAGGATTACATCCCAAGATCTCGGAGCCGAGCCCTCC 1462
QY 420 smGluIleValGlyGluIleThrSerIleAsnSerHisAlaGluLeuGlyLeuSerAsnL 440
| | | | | : : : : : | | | : : : : :
Db 1463 AGCAGTACGTCGCTCCCTATGAGAGCTATGACATCCACCGCCACCCACCTGTCCAACG 1522
QY 440 eupHeSer 442
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Db 1523 TGTTCTCC 1530

RESULT 12
PCT-US93-03837-2
Sequence 2, Application PC/TUS9303837
GENERAL INFORMATION:
APPLICANT: Baker, Jr., James R.
APPLICANT: Koenig, Ronald J.
TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03837
FILING DATE: 19930422
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lemak, Anna M.
REGISTRATION NUMBER: 33006
REFERENCE/DOCKET NUMBER: 2115-00658PPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 641-1600
TELEFAX: (313) 641-0270
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3048 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Mature
TISSUE TYPE: Thyroid gland (from patients with
tissue type: Grave's disease)
IMMEDIATE SOURCE:
CLONE: pHPPO-2.8
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 2pter-q11
PUBLICATION INFORMATION:
AUTHORS: Kimura, S.
AUTHORS: Kotani, T.
AUTHORS: McBride, O. W.

QY 84 AspSerSerValIleLeuValProPheThrGlnCysPheAlaGluArgMetThrLeuHis 103
| | | | | : : : : : | | | : : : : :
Db 393 GAAACTCAACATCATCAGCATCC---AACGATGCTTATCAGAGATCTGCTGAGCAT 449
QY 104 Tyr-----HisGlnGluLeuAspAspPyrThrPheAsnThr 114
| | | | | : : : : : | | | : : : : :
Db 450 CATTGCAACATGCTGTGATGTCCTTACATGCTGCCCAAAATGCGCAACACCTTG 509
QY 115 ProGluValGluThrArgValProHisPheGlySerThrAsnSerLeuValLeuAsn 134
| | | | | : : : : : | | | : : : : :
Db 510 CCTGGCGAACAATACAGGCCCATCC-----AGAGCTTGCACAAACAGAGA 557
QY 135 Pro-----ArgLeuLysHisIleThrGlyTyrMetAlaProLeu-ValAspSe 150
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Db 558 CCACCCGATGAGGCGCTCCCAACAGCGCCCTGGCAGCATGCTCCCTCCAGTC----- 612
QY 150 rLeuGlnLysLeuGlyTyrAlaAspGlyGluThrIlePheGlyAlaProTyrAspPheAr 170
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Db 613 -----TATGAGAGCGC-----TTCACTCAGCCCGGAGCTGGAA 647
QY 170 gTyrGlyLeuAlaAlaGluGlyHisProSerGlnValGlySerLysPheLeuLysAspLe 190
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Db 648 CCGGCGCTCTGTACAAAGGCTTCCCACTGCCCGGTCGGAGAGTCAACAAGCATGT 707
QY 190 uLysAsnLeuIleGluGluAlaSerAsnSerAsnAsnGlyLysProValIleLeuLeuSe 210
| | | | | : : : : : | | | : : : : :
Db 708 CATTCAAGTTTCAATGAGGTTGTACAGATGATGACCGCTATTCCTGACCTCTGATG-- 765
QY 210 rHisSerLeuGlyGlyLeuPheValLeuGlnLeuLeuAsnArgAsnProPheSerTyrPr 230
| | | | | : : : : : | | | : : : : :
Db 766 -----GCATG-- 771
QY 230 gLysLysPheIleLysHisPheIleAlaLeuSer-----AlaProTr 244
| | | | | : : : : : | | | : : : : :
Db 772 -GGACATATCATCGACACAGACATCGCTTCACACACAGACACAGCAAGAGCTGCTT 830
QY 244 pGlyGlyAlaIleAspGluMetTyrThrPheAlaSerGlyAsnThrLeuGlyValProLe 264
| | | | | : : : : : | | | : : : : :
Db 831 CGGGGAGGGGCTACTGTCAGATGACTGTGAGAACCAAAACCA----- 876
QY 264 uValAspProLeuValArgAspGluGlnArgSerSerGluSerAsn-----LeuTr 282
| | | | | : : : : : | | | : : : : :
Db 877 -TGTTTTCCCATACAACTCCGAGAGGCGCGCGCGCGGACCGCTGTCTGCG 935
QY 282 pLeuLeuProAsnProLysIlePhe-----GlyProGlnLysProIl 296
| | | | | : : : : : | | | : : : : :
Db 936 -CTTCTACG-----CTCTTGGCGCGCTGGCGGACCGGAGACCAAGCGCGCTCT 985
QY 296 eValIleThrProIle-----ArgProTyrSerAlaHisAspMetValAspPheLeuLy 314

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Db      986 T--TGGGAACCTGTCCACGGCCGCAACCCGCGGAGAGATGACGGGTTGACTTC 1042
Qy      314 s-AspIleGly----- 317
Db      1043 TGGACGGGTCCACCGTGTATGGACGCTCCCGCCCTAGAGAGACAGCTCGGAACTGGA 1102
Qy      318 --PheProGluGlyValTyrProTyrGluThrArgIle-----L 330
Db      1103 CCAATGGCCGAAGGGCTGCTCCGCTCCACGGCGGCTCCGGAGCTCCGGCCGCTAC 1162
Qy      330 eupProLeuIleGlyAsnIleLysAlaProGluValProIleThrCysIleMetGlyThrG 350
Db      1163 TGCCTTCCTGTG-----CCGCCACGCGGCGCTGCGCGCTGCGCGCCGAGCCCG 1210
Qy      350 LValGlyThrLeuGluThrLeuPheTyrGlyLysGlyAspPheAspGluArgProGlu 370
Db      1211 GCATC-----CCCGGAG 1222
Qy      370 IeserTyrGlyAsp-----GlyAspGlyThrValAsnLeuVal---SerLeuL 385
Db      1223 AGACCCCGGGCCCTGCTCTCTCGGAGACGGCCGCGCCAGCGAGGTCCCTCCCTGA 1282
Qy      385 euAlaLeuGlnSerLeuTyrPlySgluLysAsnGln----- 397
Db      1283 CGGCACGTGCACACGCTGTGCTGCGGAGACACCGCTGCGCGCGCTCAAGGCC 1342
Qy      398 -----TyrLeuLysValValLysIleAspGlyValS 408
Db      1343 TCAATGGCGACGTGAGCGCGGACCGCTGTACAGAGGCGCGCAAGGTCTGGCGCTC 1402
Qy      408 erHisThrSerIle---LeuLysAspGluVal-----AlaLeuA 420
Db      1403 TGCACGACATCATACCTGTAGGATATACATCCACAGATCTCTGGACCCAGGCTTCC 1462
Qy      420 snGluIleValGlyLysIleThrSerIleAsnSerHisAlaGluLeuGlyLeuSerAsnL 440
Db      1463 AGCAGTACGTGGTCCCTATGAAAGCTATGACTCCACCGCAACCCCACTGTGTCAACG 1522
Qy      440 eupPheSer 442
Db      1523 TGTCTCC 1530

RESULT 13
; Sequence 256, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
;            Burland, Valerie
;            Perna, Nicole T.
;            Plunkett, Guy
;            Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955

```

```

; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296,95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 256:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9510 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 256:
US-09-453-702B-256

Alignment Scores:
Pred. No.: 4.55 Length: 9510
Score: 96.00 Matches: 91
Percent Similarity: 34.75% Conservative: 64
Best Local Similarity: 20.40% Mismatches: 151
Query Match: 4.11% Indels: 141
DB: Gaps: 25

US-09-857-612a-14 (1-443) x US-09-453-702B-256 (1-9510)
Qy      50 LeuGluAlaArgLeuThrAsnGlnTyrLysProSerThrPheIleCysGluSerTyr 69
Db      8146 TTAGAGTAAATAATAGATATGTTACAAAGATAGTAAATTACATGGGAACGAT-- 8202
Qy      70 ProLeuIleLysLysAsnGlyTyrPheArgLeuThrPheAspSerSerValIleLeu 89
Db      8203 -----GGTGAATATGCTGTGA 8217
Qy      90 AlaProPheThrGlnCysPheAlaGluArgMetThrLeuHisTyrHisGlnGluLeuAsp 109
Db      8218 TCACCT-----GAAGATAGAAATTCT--CATCTGAGATTAGAT 8253
Qy      110 -----AspTyrPheAsnThrProGlyValGluThrArgVal----- 121
Db      8254 GGGTTTAAATTATTTTTCACAAACCGAGTTAGATATCTCAATATGACTCATTTTCATAT 8313
Qy      122 -----ProHisPheGlySerThrAsnSer-----LeuLeuTyrLeuAsn 134
Db      8314 TTATATGATATATTTTCAGATGCTGTGATGTGATGATATTAAGCTTCACTCTCAAC 8373
Qy      135 ProArgLeuLysHisIleThrGlyTyrMetAlaProLeu-----ValAspSer 150
Db      8374 AGAGAAACAAAGCAATATACACCAACATCGTATTTCTTAAAGATACTTATTAGACTCA 8433
Qy      151 LeuGlnLysLeuGlyTyrAlaAspGlyLys-----ThrLeuPheGlyAla 165
Db      8434 TTGCTTAAACAGATACATGACACAGAGAAAGATATATATTCCTGATTTTGATGTCA 8493
Qy      166 Pro-----TyrAspPheArgTyrGlyLeuAlaAlaGlu 176
Db      8494 CCGTACACTTCACAGCGACATATATAGGCATCATTTAGAAATAGTTCCGGGAATAG 8553
Qy      177 Gly---HisProSerGlnValGlySerLysPheLeuLysAspLeuLysAsnLeuIleGlu 195
Db      8554 ACATTGTATCCATCAGAGAACTGTAAATATTCAT--AAGCACTCCAAAGAAATATTAG 8612
Qy      196 Glu-----AlaSerAsnSerAsnAsnGlyLysProVal 206
Db      8613 CAATATGATGTGATTAACATATGTTATGTTCTCCCAAAAAACAAAGAAACAAAT 8672
Qy      207 IleLeuLeuSerHisSer-----LeuGlyGlyLeuPheValLeuGln 220
Db      8673 ATC-----CATAGTTAGTTAAATAGCAATATCAAAATAGATATTTGATGTCCGG 8723
Qy      221 LeuLeuAsnArgAsnProProSerTyrPheArgLysLysPheIleLysHisPheIleAla--- 239

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Db      8724 AGTAATGACGCGAACAATCAAGATTTTTCATCTAAATTAATTCAGCGATTTATTTAAAC 8783
QY      240 ---LeuSerAlaProTrp-GlyGlyAlaIleAspGluMetTyr-ThrPheAlaSerGly-- 257
Db      8784 AACCTCAAAACATCATGCGTGGCTGGTGGTATTTTAAAGATTTTATAATATACAG 8843
QY      258 -----AsnThrLeuGlyValProLeu----- 264
Db      8844 GTGCAATATATATCTACTTATATACAGTTCCTATTTGATTAATTAATTCACACATAG 8903
QY      265 -----ValAspProLeuLeuValArg---AspGluGlnArgSerSerGluSerAsnLe 281
Db      8904 AATTAATATTAACCCATGCGGATGAAGATACAGAAACAGTCAAGTCAAGTCAAGTCAAG 8963
QY      281 uTrpLeuLeuProAsnPro-----LysIlePheGlyProGluLysProIleVal11 298
Db      8964 GTTTTTCATCCCTTCCTTATATACATGATTAATTTATCTTCGCAATATCCACTTACTC 9023
QY      298 eThrProIleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIleGlyPh 318
Db      9024 TAACATATCCCTTCCTTATATACATGATTAATTTATCTTCGCAATATCCACTTACTC 9077
QY      318 eProGluGlyValTyrProTyrGluThrArgIleLeuProLeuIleGlyAsnIleLysAl 338
Db      9078 TAGAAATCCAAAGTATTCGAT-----TTACAGAACAAAT----- 9111
QY      338 aProGluValProIleThrCysIleMetGlyThrGlyValGlyThrLeuGluThrLeuPh 358
Db      9112 -----ATTATCAATAGATATATACATACCTGTTCT----- 9141
QY      358 eTyrGlyLysGlyAspPheAspGluArgProGluIleSerTyrGlyAspGlyLysAl 378
Db      9142 -----GAGTATGCTGCAAAACACGCTAT 9164
QY      378 rValAsnLeu---ValSerLeuLeuAlaLeuGlnSer-----LeuTyrLysGluGly 395
Db      9165 TGCCATATATGCTATATATATATACGATATCGACATGCTGTTGCTGCAAAAGAAAG 9224
QY      395 sAsnGlnTyrLeuLysValValLysIleAspGlyValSerHis-----Th 410
Db      9225 TGTGGCTGAGACGATACATATAAATTGCTATATATGACGATATGAGCTTTAGCTTTAA 9284
QY      410 rSerIleLeuLysAsp 415
Db      9285 TTCATTTAGTAAGAT 9300

RESULT 14
US-09-134-001C-513
; Sequence 513, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 513
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-513

Alignment Scores:
Pred. No.: 0.626 Length: 1983
Score: 94.00 Matches: 90
Percent Similarity: 36.41% Conservative: 56

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Best Local Similarity: 22.44% Mismatches: 104
Query Match: 4.03% Indels: 151
DB: 4 Gaps: 26

US-09-857-612A-14 (1-443) x US-09-134-001C-513 (1-1983)

QY      71 LeuIleLysLysLysAsnGlyTyrPheArgLeuTyrPheAspSerSerValIleLeuAla 90
Db      502 CTGTAAGAAGAAAGACATATTCCTCAACATT----- 534
QY      91 ProPheThrGlnCysPheAlaGluArgMetThrLeuHisTyrHisGlnGluLeuAspAsp 110
Db      535 -----AATTAATATACAGACCGCTTA---TTGAATTTTACATGAATAATCCAGAC 582
QY      111 Tyr-----PheAsnThrProGlyVal 117
Db      583 TTATATCAACACCATCTAGAAAAATGAATGATTAATTAATCTTTATCAACACGCTTTA 642
QY      118 Gly-----ThrArgValProHisPheGly 125
Db      643 GAAGATTTAGCACTATCAGTACATCATTCGATGCGGTGAGTACGTACCATCT----- 696
QY      126 SerThrAsnSerLeuLeuTyrLeuAsnProArgLeuLysHisIleThr---GlyTyrMet 144
Db      697 -----AATCCT-----AAACATGTTGTATACGTGTGGATT 726
QY      145 AlaProLeuValAspSerLeuGlnLysLeuGlyTyr---AlaAspGlyGluThrLeuPhe 163
Db      727 GATGCACTTGTTATATATATTTCTTCATTAAGTTATCTGATCATGATGAACATTTATTT 786
QY      164 GlyAlaProTyrAspPheArgTyrGlyLeuAlaIleGluGlyHisProSerGluValGly 183
Db      787 AAT-----AAATATTGGCCAGCA----- 804
QY      184 SerLysPheLeuLysAspLeuLysAsnLeuIleGluGluAlaSerAsnSerAsnGly 203
Db      805 -----GACATACACTTGATGCGCTAAGAA----- 828
QY      204 LysProValIleLeuLeuSerHisSerLeuGlyGlyLeuPheValLeuGlnLeuAsn 223
Db      829 -----ATTGTACGTTCCACTATTT-----ATATGGCCAAATATGTTAATGGCG 873
QY      224 ArgAsnProProSerTyrArgLysLysPheIleLysHisPheIleAlaLeuSerAlaPro 243
Db      874 TTGATTTACCACTTCCTAAAGATTTTGGACACGCGTTGATTTTATGAAGAA----- 927
QY      244 TyrGlyGlyAlaIleAspGluMetTyrThrPheAlaSerGlyAsnThrLeuGlyValPro 263
Db      928 -----GATGTAATAATGAGTAATCTAAGATTAAT----- 957
QY      264 LeuValAspProLeuLeuValArgAspGluGlnArgSerSerGluSerAsnLeuTyrLeu 283
Db      958 GTGCTAGATCCCTATATATATATATGATGCTTATGCTGATGCGACGACGATATTAAGTTA 1017
QY      284 -----LeuProAsnProLysIlePheGlyProGlnLysProIleValIleThrPro 300
Db      1018 ATGCGGATTTACG-----TTTGGTTCGATGGC-----GTATTTACACCG 1059
QY      301 IleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIleGly---PheProG 320
Db      1060 -----GAAGCCTTGTGGAAGAACAAATTAAGATCTTGGCAATGATTTAGTAACTAGTG 1116
QY      320 IuGlyValTyrProTyrGluThrArgIleLeuProLeuIleGlyLysAsnIleLysAlaProG 340
Db      1117 AATCGACTATCTCTATATGAATAAATTTTCCACG----- 1154
QY      340 IuValProIleThrCysIle-MetGlyThrGlyValGlyThrLeuGluThrLeuPheTyr 359
Db      1155 -----CGAATTACCTGATACCAAGGTCCA----- 1179
QY      360 GlyLysGlyAspPheAspGluArgProGluIle-----SerTyr 372
Db      1180 ---AAACATGAATTTGATGAAAAAATGAAAGGATGCGGCTTGAACATGTTAAATCATTC 1236

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QY 373 GlyaspGlyaspGlythrValAlaLeuValSerLeu-----LeuAlaLeuGlnSer 389
Db 1237 AATGAT-----AATATGGAAGATTACAAATTTCTGTTGCTTATACACA 1281
QY 390 LeuThrLys-----GluGluLysAsnGlnTyrLeuLysValValLysIleAspGlyVal 407
Db 1282 GTATGGAATTTATTAGTCGTACCAACAAATAT-----ATTGATGAAACT 1326
QY 408 SerIsthrSerIleLeuLysAspGlyValAlaLeuAsnGluIleValGluIle 426
Db 1327 CAACCTGGCTTTCGAAAGATGAA---AATCAACGTGAGATGCTTGATGTA 1380
RESULT 15
US-08-716-449-1
Sequence 1, Application US/08716449
Patent No. 6103893
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment
TITLE OF INVENTION: Method for Producing Altered Starch
TITLE OF INVENTION: from Potato Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott & Aylen
STREET: Box 194, 24th Floor, Toronto-Dominion Bank Tower
CITY: Toronto
STATE: Canada M5K 1H6
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: 1MB 1.44 MB High Density Diskette
COMPUTER: COMPAQ Deskpro 590 (IBM PC compatible)
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: Word 7.0 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,449
FILING DATE: FILED CONCURRENTLY HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00634
FILING DATE: 22.03.95
ATTORNEY/AGENT INFORMATION:
NAME: Anita E. Nador
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 1552
TELEPHONE: (416) 368-2400
TELEFAX: (416) 363-7246
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: cDNA encoding starch branching enzyme
HYPOTHECAL: No
ANTI-SENSE: No
FRAGMENT TYPE:
ORIGINAL SOURCE: clone 1.2.1 and E2
ORGANISM: Solanum tuberosum
STRAIN: cv desiree
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: mature tuber
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY: lambda Zap tuber cDNA
CLONE: 1.2.1 and E2
POSITION IN GENOME:

CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE: open reading frame
NAME/KEY: starch branching enzyme
LOCATION: 44-2788
IDENTIFICATION METHOD: lone ORF with homology to other starch
IDENTIFICATION METHOD: branching enzymes
OTHER INFORMATION: complements KV832 E. coli glycogen
OTHER INFORMATION: branching enzyme mutant
US-08-716-449-1
Alignment Scores:
Pred. No.: 1.96 Length: 3128
Score: 92.50 Matches: 88
Percent Similarity: 32.48% Conservative: 65
Best Local Similarity: 18.68% Mismatches: 151
Query Match: 3.96% Indels: 167
DB: 3 Gaps: 24
US-09-857-612a-14 (1-443) x US-08-716-449-1 (1-3128)
QY 35 AsnLeuAspProLeuIleLeuIleProGlyAsnGlnLeuGluAlaArgLeu 54
Db 341 AATTGGATGCA-----ACTTGGAACTTATCTA 370
QY 55 ThrAsn-----GluTyrLysProSerThrPheIleCysGluSerThr 68
Db 371 GATCACTTCACACACAGATGAGATGTGTCATCAGAAATGCTATTGAAATAATAT 430
QY 69 Tyr---ProLeuIleLysLysAsnGlyThrPheArgLeuThrPhe-----Asp 84
Db 431 GAGGAGACCCCTTGAGGATTTGCTCAGCATTTAATAATTGGATTCACAGGAGAAAT 490
QY 85 SerSerValIleLeuAlaProPheThrGlnCysPheAlaGluArgMetThrLeu----- 102
Db 491 GGTTCATAGTCTATCTGGAATGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550
QY 103 -----HisTyrHisGlnGluLeuAspAspTyr----- 111
Db 551 TTCATGATGATGAGACGTTCTTACCATGATGAGAGACCGATTGGTGTGGAGT 610
QY 112 PheAsnThrProGlyValGluThrArg-----ValProHisPheGlySerThrAsnSer 129
Db 611 ATTGAATTCCTGATGTTGACAGTACGATGATCCACAC-----AATCC 658
QY 130 LeuLeuTyrLeuAsnProArgLeuLysHisIleThrGlyTyrMetAlaProLeuValAsp 149
Db 659 AGAGTTAGTTT-----CGTTTCAACATGATGATGAGAGTGGGTGATCGTATCCCT 712
QY 150 SerLeuGlnLysLeuGlyTyrAlaAspGlyGluThrLeuPheGlyAlaProTyrAsp--- 168
Db 713 GCTTGATTAAGTATGATGCCACTGCAGACGCC---ACAAAGTTTGCACGACCATATGATG 769
QY 169 -----PheArgTyrGlyLeuAlaAla--- 175
Db 770 GTCTACTGGACCCACACACCTTCAGAAAGTACCATCTCAATACCTCGCCCTCCCAAA 829
QY 176 -----GluGlyHisProSerGlnValGlySer----- 184
Db 830 CCCCAGCCCGACGATTCAGACATGTCGCGCATGACAGCTGACAGCCAGTGA 889
QY 185 -----LysPheLeuLysAspLeuLysAsnLeuIleGluGluAlaSerAsnSer 200
Db 890 AATTCGTATCGTGAAGTTTGACAGATGATGTTTACCTCGGATT---AAGCAAAATTAATAT 946
QY 201 AsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyLeuPheValLeuGln 220
Db 947 AATACTGTCAGATGATGACCATATATGACATTTCTTACTGATCTATTTGGATATAT 1006
QY 221 LeuLeuAsnArgAsnProProSerThrPargLysLysPheIleLysHisPheIleAlaLeu 240
Db 1007 GTTACAAC-----TTTTCGCTGTG 1027

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OY 241 SerAlaProTPrGlyGlyAlaIleAspGluMetTyrThrPheAlaSerGlyAsnThrLeu 260
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Db 1028 AGCAATAGATATATGAAACCGAGACCTAAAGTATCTGTATAGATAAGACATACCTTG 1087
    |||
OY 261 GlyValProLeuValAspProLeuValArgAspGluGlnArgSerSerGluSerAsn 280
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Db 1088 GGTATA----- 1093
OY 281 LeuTrpLeuLeuProAsnProLysIlePheGlyProGlnLysProIleValIleThrPro 300
    |||
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    :|:|:|
Db 1094 -----CAGCTTCGTGGATGTA 1111
OY 301 IleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIleGlyPheProGlu 320
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Db 1112 GTTCACAGTCATCAGACATAATATGTCACATGAGCCTCAAT-----GGCTTT----- 1159
OY 321 GlyValTyrProTyrGluThrArgIleLeuProLeuIleGlyAsnIleLysAlaProGln 340
    |||
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Db 1159 ----- 1159
OY 341 ValProIleThrCysIleMetGlyThrGlyValGlyThrLeuGluThrLeuPheTyrGly 360
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Db 1160 -----GATATTGCCAAGGTTTCACAGATCCTACTTTCATGCT 1198
OY 361 LysGlyAsp-----PheAspGluArgProGluIleSerTyrGlyAsp 374
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Db 1199 ---GGAGACCGAGGATACCATAGTTGTGGATACGAG---CTGTCAACTATGCCAAT 1252
OY 375 GlyAspGlyThrValAsnLeuValSerLeuLeuAlaLeuGlnSerLeuTrpLysGlu 394
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Db 1253 TGGGAG-----GTCTCTGCTTCCCTTCCACTTCAGGTGGCTAGAAAGAG 1303
OY 395 LysAsnGlnTyrLeuLysValValLysIleAspGlyValSerHisThrSerIleLeuLys 414
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Db 1304 TATTAAC-----TTTGACGATTTGATTTGATGCAATACTTCTATGCTGATGTTCAAT 1357
OY 415 AspGluValAlaLeu-----AsnGluIleValGlyGluIleThrSer 428
    :|:|
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Db 1358 CATGCAATCAATATGAGATTACAGGAACATAATAGATATTTCACGCGGCTACAGAT 1417
OY 429 IleAsnSerHisAlaGluLeuGlyLeuSerAsn 439
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Db 1418 GTTGATGCTGTGCTATTATTAAATGTTGCCAAT 1450
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Search completed: February 15, 2003, 15:22:53
Job time : 77 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: February 15, 2003, 14:56:22 ; Search time 65 Seconds

(without alignments)
3471.237 Million cell updates/sec

Title: US-09-857-612A-14

Perfect score: 2333

Sequence: 1 MKKEDEGKIEVATLVTV.....GETTSINSHALGSLNLFSG 443

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 424239 segs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-TRANS-human40.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
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-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1367	58.6	9	US-09-938-842A-376
2	610	26.1	9	US-09-978-295A-156
3	610	26.1	9	US-09-978-697-156
4	610	26.1	9	US-09-978-192A-156

5	610	26.1	2680	9	US-09-999-832A-156	Sequence 156, App
6	541	23.2	1744	9	US-09-978-189-156	Sequence 156, App
7	541	23.2	1744	10	US-09-919-497-30	Sequence 30, Appl
8	541	23.2	1744	10	US-09-880-107-2245	Sequence 2245, Ap
9	433	18.6	1048	9	US-09-998-059-8	Sequence 8, Appl1
10	433	18.6	1059	9	US-09-998-059-20	Sequence 20, Appl
11	433	18.6	1080	9	US-09-998-059-27	Sequence 27, Appl
12	411.5	17.6	2180	9	US-10-001-054-7	Sequence 7, Appl1
13	169.5	7.3	248	10	US-09-923-876-2515	Sequence 2515, Ap
14	151.5	6.5	527	10	US-09-967-701-5139	Sequence 5139, Ap
15	142	6.1	1482	9	US-09-938-842A-1935	Sequence 1935, Ap
16	134	5.7	266	10	US-09-960-352-2549	Sequence 2549, Ap
17	112	4.8	900	9	US-09-738-626-94	Sequence 94, Appl
18	110.5	4.7	393	10	US-09-960-352-9177	Sequence 9177, Ap
19	104	4.5	954	9	US-09-938-842A-2479	Sequence 2479, Ap
20	103.5	4.4	1014	9	US-09-738-626-2470	Sequence 2470, Ap
21	101	4.3	2305	10	US-09-896-578-1	Sequence 1, Appl1
22	100.5	4.3	1029	10	US-09-896-578-3	Sequence 3, Appl1
23	100.5	4.3	1533	10	US-09-729-402-23	Sequence 23, Appl
24	100	4.3	20633	10	US-09-070-927A-276	Sequence 276, App
25	97.5	4.2	1041	9	US-10-027-805-24	Sequence 24, Appl
26	97.5	4.2	1041	10	US-09-903-410-24	Sequence 24, Appl
27	97.5	4.2	3042	9	US-09-738-626-1156	Sequence 1156, Ap
28	97.5	4.2	249487	9	US-10-026-188-3	Sequence 3, Appl1
29	97	4.2	1014	9	US-09-738-626-2192	Sequence 2192, Ap
30	96.5	4.1	1854	9	US-09-738-626-2266	Sequence 2266, Ap
31	96	4.1	9510	9	US-10-114-170-256	Sequence 256, App
32	95.5	4.1	1868	9	US-09-981-353-18	Sequence 18, Appl
33	95	4.1	263	10	US-09-878-574-6764	Sequence 6764, Ap
34	94	4.0	2416	10	US-09-748-739A-5	Sequence 5, Appl1
35	93.5	4.0	235	10	US-09-960-352-2308	Sequence 2308, Ap
36	93	4.0	3045	8	US-08-910-386A-16	Sequence 16, Appl
37	92.5	4.0	957	9	US-09-938-842A-316	Sequence 316, App
38	92	3.9	2191	10	US-09-729-402-22	Sequence 22, Appl
39	92	3.9	6544	10	US-09-764-847-1544	Sequence 1544, Ap
40	91.5	3.9	1170	10	US-09-815-242-6314	Sequence 6314, Ap
41	91.5	3.9	3029	9	US-09-834-975-811	Sequence 811, App
42	91	3.9	1239	9	US-09-938-842A-2482	Sequence 2482, Ap
43	91	3.9	1344	9	US-09-938-842A-2137	Sequence 2137, Ap
44	90	3.9	2381	10	US-09-880-107-2271	Sequence 2271, Ap
45	90	3.9	2416	10	US-09-748-739A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-938-842A-376
: Sequence 376, Application US/0993842A
: Patent NO. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: SAME-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME-REGULATED GENES OF USE
: FILE REFERENCE: SCRIPT300-3
: CURRENT APPLICATION NUMBER: US/09/938, 842A
: PRIOR FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227, 866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264, 647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300, 111
: NUMBER OF SEQ ID NOS: 2001-06-22
: SEQ ID NO 376
: LENGTH: 1242
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-376
Alignment Scores:

Pred. No.: 7,56e-155 Length: 1242
 Score: 1367.00 Matches: 258
 Percent Similarity: 77.26% Conservative: 58
 Best Local Similarity: 63.08% Mismatches: 83
 Query Match: 58.59% Indels: 10
 DB: 9 Gaps: 4

US-09-857-612A-14 (1-443) x US-09-938-842A-376 (1-1242)

25 LeuSerLeuLeuCySerThrCysGlyAlaSerAsnLeuAspProLeuIleLeuIleProGly 44
 1 ARGACCTGATGTGTCACCTGTCGGGTAGCAACGTCCTGATTTCTGGTTCAGCA 60
 45 AsnGlyGlyAsnGlnLeuGluAlaArgLeuThrAsnGlnTyrLysProSerThrPheIle 64
 61 AACCGAGGTACACGCTAGACGATGACGCTGACAGCAAGATACAAAGCAAGTACTGCTCG 120
 65 CysGluSerTrp---TyrProLeuIleLysLysAsnGlyTyrPheArgLeuTrpPhe 83
 121 TGTACGAGCTGTTATATCCGATTCTAAGAGAGAGTGCTGGATGTTTAGCGTATGCTTC 180
 84 AspSerSerValIleLeuAlaProPheThrGlnCysPheAlaGluArgMetThrLeuHis 103
 181 GATGCGACGAGTGTATTTGCTCCCTCACCAGGTGCTTCAGCGATGATGATGATGATGAC 240
 104 TyrHisGlnGluLeuAspAspTyrPheAsnThrProGlyValGluThrArgValProHis 123
 241 TATGACCCCTGATTTGATGATACCAAAATGCTCCCTGCTCCAAACCGCGGTCTCAT 300
 124 PheGlySerThrAsnSerLeuLeuTyrLeuAsnProArgLeuLysHisIleThrGlyTyr 143
 301 TTGGGTTCAACAAATCACTTCTATACCTCGACCCCTGCTCCGAGATGCCACATCTTAC 360
 144 MetAlaProLeuValAspSerLeuGln---LysLeuGlyTyrAlaAspGlyGluThrLeu 162
 361 ATGGAACATTTGGTGAACCTCTAGAGAAAATAAGGGGTATGTTACAGCAACCAACATC 420
 163 PheGlyAlaProTyrAspPheArgTyrGlyLeuAlaIleGluGlyHisProSerGlnVal 182
 421 CTAGGAGCTCCATATGATTTCAAGTACGGCTGCTGCTCGGCGCACCGCTCCGTGA 480
 183 GlySerLysPheLeuLysAspLeuLysAsnLeuIleGluGluAlaSerAsnSerAsnAsn 202
 481 GCCTACACATCTCTACAAAGACCTCAAAACATTTGGTGGAAAAAATGACGCGAAGCGAA 540
 203 GlyLysProValIleLeuLeuSerHisSerLeuGlyGlyLeuPheValLeuGlnLeu 222
 541 GGAAGGCCAGTATCTCTCTCCATAGCCTAGAGAGACTTTGCTCTCATTTCTCTC 600
 223 AsnArgAsnProProSerTrpArgLysLysPheIleLysHisPheIleAlaLeuSerAla 242
 601 AACCTACACCCCTTACATGAGCGCGCAGTACATCAACACTTTGTTCTCAGCTCGTGG 660
 243 ProTrpGlyGlyAlaIleAspLeuLeuTyrTrpPheAlaSerGlyAsnThrLeuGlyVal 262
 661 CCATGGGGGGGAGCATCTCTCAGATGAGACATTTGCTTGGGCAACACATCGGTGTC 720
 263 ProLeuValAspProLeuLeuValArgAspGluGlnArgSerSerGlnSerAsnLeuTrp 282
 721 CCTTTAGTTAACCTTTGCTGTCAGCGCATTCAGAGAGACTCCGAGAGTAAACCAATGG 780
 283 LeuLeuProAsnProLysIlePheGlyProGln---LysProIleValIleThrProIle 301
 781 CTACTTCATCTACCAAAAGTGTTCACAGCAGACACTAAACCCCTGTCTACTCCCGAG 840
 302 ArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIleGlyPheProGluGly 321
 841 GTTAACTACACAGCTTAGAGATGATCGTCTTTTCCAGACATTTGGATTTCTCACAAAGA 900
 322 ValTyrProTyrGluThrArgTyrLeuProLeuIleGlyAsnIleLysAlaProGlnVal 341
 901 GTTGTGCTTACAGACAGAGAGTGTGCTTTAACAGAGAGACTGATGACTCCGGGAGTG 960

342 ProIleThrCysIleMetGlyThrGlyValGlyThrLeuGluThrLeuPheTyrGlyLys 361
 961 CCAGTCACTTGGTATATATGAGAGAGATTTGATACACCGAGGTTTGTATGAGAAAA 1020
 362 GlyAspPheAspGluArgProGluIleSerTyrGlyAspGlyAspGlyThrValAsnLeu 381
 1021 GGAGATTTGATGATGACACACGAGATTAAGTATGAGATGAGATGGACGGTTAATTTTG 1080
 382 ValSerLeuLeuAlaLeuGlnSerLeuTyrLysGluGluLysAsnGlnTyrLeuLysVal 401
 1081 GCGAGCTTGTAGCAGCTTGTG-----AAAGTCATAGCTTGAACACC 1119
 402 ValLysIleAspGlyValSerHisThrSerIleLeuLysAspGlyValAlaLeuAsnGlu 421
 1120 GTAGACATTTGATGAGATTTGCGATACATCTATATTAAGACAGAGATCGACTTAAGAG 1179
 422 IleValGlyGluIleThrSerIleAsn 430
 1180 ATTATGACGAGATTTCAATTTATTAAT 1206

RESULT 2
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 Sequence 156, Application US/0978295A
 Patent No. US70020156006A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Goddard, Audrey E.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paonli, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C11
 CURRENT APPLICATION NUMBER: US/09/978, 295A
 PRIOR FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
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 PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-04-21	

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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 3,76e-63 Length: 2680
Score: 610.00 Matches: 141
Percent Similarity: 54.578 Conservative: 80
Best Local Similarity: 34.818 Mismatches: 156
Query Match: 26.154 Indels: 28
Gaps: 12

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Db CTTCTGCTGCTGCTAAATGCTGCTGCGGACCCAGCGCTCCCGCGGAGCTGACCCCCCA 137
QY 39 LeuIleLeuLeuLeuProGlyAsnGlyGlyAsnGlnLeuGlnAlaArgLeuThrAsnGlnTyr 58
Db GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 188
QY 59 LysPProSerThr-----PheIleCysGlySerTyrTyrProLeuIleLysLysAsn 76
Db AACGCGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 230
QY 77 GlyTyrPheArgLeuThrPheAspSerSerValIleLeuAlaProIleThrGlnCysPhe 96
Db ACCTACTGTCACATCTGCGTGAACCTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 290
QY 97 AlaGluArgMetThrLeuHisTyrHisGlnGlnLeuLeuAspArgTyrThrPheAsnProGly 116
Db ATTGACAAATATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 350
QY 117 ValGluThrArgValProHisPheGlySerThrAsnSerLeuLeuLeuAsnProArg 136
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QY 137 LeuLysHisIleThrGlyTyrIleLeuAlaProLeuValAspSerLeuGlnLysLeuGlyTyr 156
Db AAAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 470
QY 157 AlaAspGlyGluThrLeuPheGlyAlaProTyrAspPheArgTyrGlyLeuAlaIleGlu 176
Db ACACGGGGTGAAGATGCTCGAGGGGCTCCCTATGACTGCGCGCAGCC----- 518
QY 177 GlyHisProSerGlnValGlySerLysPheLeuLysAspLeuLysAsnLeuIleGln 196
Db CCAATATGAAGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 569
QY 197 AlaSerAsnSerAsnAsnGlyLysProValIleLeuLeuSerHisSerLeuGlyGlyLeu 216
Db ATGTACACACCTGTATGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626
QY 217 PheValLeuGlnLeuLeuAsnArgAsnProProSerTyrArgLysLysPheIleLysHis 236
Db TACACGCTCTACTTCTGTGAGCGGCGCGCAGGCTGGAAGACAAATATCCGGGCC 686
QY 237 PheIleAlaLeuSerAlaProTyrGlyGlyAlaIleAspGluMetTyrThrPheAlaSer 256
Db TTTCGTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 746
QY 257 GlyAsnThrLeuGlyValProLeuValAspProLeuLeuValArgAspGlnIleArgSer 276
Db GGAGACAAACACCGGATCCAGTCCAGGCGCGCTGGAAGATCGGAGACAGCGGCTCA 806
QY 277 SerGluSerAsnLeuThrLeuLeuProAsnProLysIlePheGlyProGlnProIle 296
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Db 807 GCTGTCTCCACGACGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 866
QY 297 ValIleThrProIleArgProTyrSerAlaHisAspMetValAspPheLeuLysAspIle 316
Db GTTCACACACCCACCATCACTGACACACGTGGGAGTACCAGGATTTCTTCCAGGACATC 926
QY 317 GlyPheProGlyGly--ValTyrProTyrGluThrArgIleLeuProLeuIleGlyAsn 335
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Db ACAGTCCACCTGGCGCTGCGAGTGCACCTGCTTATGAGTACGCGCTCCACACAGGAC 1040
QY 356 ThrLeuPheTyrGlyLysGlyAspPheAspGluArg--ProGluIleSerTyrGlyAsp 374
Db TCTCTTCTACTAT-----GAGACCTTCCCTGACCGCTGACCTTAATATCTGCTTGGTAC 1094
QY 375 GlyAspGlyThrValAsnLeuValSerLeuLeuAlaLeuGlnSerLeuThrLysGlnGlu 394
Db GCGGATGTACTGCTGTAAGTGAAGTGGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTG 1151
QY 395 LysAsnGlnTyrLeuLysValValLysIleAspGlyValSerHisThrSerIleLeuLys 414
Db CAGGACACCAAGTGTGTGCGAGGAGTGCAGGACGAGCAGCAGCAGCAGCAGCAGCAGCAG 1211
QY 415 AspGluValAlaLeu 419
Db AACGCCACCAACCTG 1226

RESULT 4
US-09-978-192A-156
; Sequence 156, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978, 192A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 1997-11-21	PRIOR APPLICATION NUMBER: 60/077450
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Oy 78 TrpPheArgLeuThrPheAspSerSerValILELeuAlaProPheThcInLcysPheLa	97
Db 508 TTCCTTCACACATCTGGCTGGATCTCAACATGTTCCTACCCCTGGGGGTAGACTGCGATC	567
Oy 98 GluArgMetThrLeuHisTyrHisGLnLLeuAspAspTyrPheAsnThrProGlyVal	117
Db 568 GATAAACACCAAGGTCGTCTCAACACCGAGACTCGGGCTGTGTCCACAGCCCTGTGTTC	627
Oy 118 GluThrArgValProHisPheGlySerThrAsnSerLeuLeuTyrLeuAsnProArgLeu	137
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Oy 258 AsnThrLeuGlyValILEuLeuValAspProLeuLeuValArgAspGLnGLnArgSerSer	277
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Oy 376 AspGlyLutThrValAsnLeuValSerLeuLeuAlaLeuGLnSerLeuTTrpLysGLnGLy	395
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: GENERAL INFORMATION:				
: APPLICANT: Horne, Darci T.				
: APPLICANT: Vockley, Joseph G.				
: APPLICANT: Scherf, Uwe				
: APPLICANT: Gene Logic, Inc.				
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer				
: FILE REFERENCE: 44921-5028-Y0				
: CURRENT APPLICATION NUMBER: US 60/880,107				
: CURRENT FILING DATE: 2001-06-14				
: PRIOR APPLICATION NUMBER: US 60/211,379				
: PRIOR FILING DATE: 2000-06-14				
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: PRIOR FILING DATE: 2000-10-02				
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QY	118	GluThrArgValProHisPheGlySerThrAsnSerLeuLeuTyrIleAsnProArgLeu	137	
Db	628	CAGATCCCGCGTCCCTGGCTTTGGCAAGACACTCTGTGTGGAGTACCTGGACAGC-----	661	
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QY	158	AspGlyGluThrLeuPheGlyAlaProTyrAspPheArgTyrGlyLeuAlaIleGlnGly	177	
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PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/US01/27099
PRIOR FILING DATE: 2001-08-29
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SEQ ID NO 7
LENGTH: 2180
TYPE: DNA
ORGANISM: Homo Sapien
US-10-001-054-7

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Best Local Similarity:	36.08%	Mismatches:	97
Query Match:	17.64%	Indels:	15
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US-09-857-612A-14 (1-443) x US-10-001-054-7 (1-2180)

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QY 187 LeuLysAspLeuLysAsnLeuIleGluGluAlaSerAsnSerAsnGlyProVal 206
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DB 43 GTGGCC--CTCCGCGAGATGATCGAGAGATGACCTGATGAGGCGC--CCGTC 96
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DB 337 AACTACACATGTCACCTGAGAGAGTTCGTCGACAGACACCCAAATGACATACACCTG 396
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      |||:|||||
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QY 405 AspGlyValSerHisThrSerIleLeuLysAspGluValAlaLeu 419
      |||:|||||
DB 682 CCAGCGACGAGACATGATGATGTGGCCACGACACACCCCTG 726
      |||:|||||

```

RESULT 13

```

US-09-923-876-2515
; Sequence 2515, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Ialoudi, Raghuath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON

```

```

; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 2515
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700160724H1
US-09-923-876-2515

```

Alignment Scores:

Pred. No.:	9,26e-12	Length:	248
Score:	169.50	Matches:	33
Percent Similarity:	67.16%	Conservative:	12
Best Local Similarity:	49.25%	Mismatches:	21
Query Match:	7.27%	Indels:	1
DB:	10	Gaps:	1

US-09-857-612A-14 (1-443) x US-09-923-876-2515 (1-248)

```

QY 150 SerLeuGlnLysLeuGlyTYrAlaAspGlyGluThrLeuPheGlyAlaProTyrrAspPhe 169
      |||:|||||
DB 51 GCACCTGAGACATGGATGGATCCGAGACGAGACACCATGTCGAGCGCCCTACGACTTC 110
      |||:|||||

QY 170 ArgTYrGlyLeuAlaAGluGlyHISProSerGlnValGlySerLysPheLeuLysAsp 189
      |||:|||||
DB 111 CGCTACCGCGCGCGCTCCCGGCGACAGCTCCGAGGTGATCTCCGCTACCAAGAG 170
      |||:|||||

QY 190 LeuLysAsnLeuIleGluGluAlaSerAsnSerAsnGlyProValIleLeuLeu 209
      |||:|||||
DB 171 CTGATGAGAGCTGTGCGAGCGCGCAAGCGAGAGACCCGAAAGAGCGCTGATC--CTC 227
      |||:|||||

QY 210 SerHisSerLeuGlyGlyLeu 216
      |||:|||||
DB 228 GGCCACAGCTTCGCGCGCATG 248
      |||:|||||

```

RESULT 14

```

US-09-867-701-5139
; Sequence 5139, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agilate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121, 497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5139
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(527)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-5139

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Alignment Scores:

Pred. No.:	4,56e-09	Length:	527
Score:	151.50	Matches:	44
Percent Similarity:	51.19%	Conservative:	42
Best Local Similarity:	26.19%	Mismatches:	77

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 15, 2003, 14:02:12 ; Search time 1680 seconds
(without alignments)
4270.596 Million cell updates/sec

Title: US-09-857-612a-14
Perfect score: 2333
Sequence: 1 MKKEDEGLKIEVATLVTVT.....GETTSINSHAEGLSLNLSFG 443

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09857612/runat_11022003_111818_29838/app_query.fasta_1.583
-DB=EST -OFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=Pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857612.ecgn_1_1.899_etrunat_11022003_111818_29838 -NCPU=6 -ICPU=3
-NO_XLUPX -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database :
EST :
1: em_estba :
2: em_estlum :
3: em_estlin :
4: em_estmu :
5: em_estov :
6: em_estpl :
7: em_estro :
8: em_hlc :
9: gb_est1 :
10: gb_est2 :
11: gb_hlc :
12: gb_est3 :
13: gb_est4 :
14: gb_est5 :
15: em_estfun :
16: em_estom :
17: gb_gss :
18: em_gss_hum :
19: em_gss_inv :
20: em_gss_pln :
21: em_gss_vrt :
22: em_gss_fun :
23: em_gss_mam :
24: em_gss_mus :
25: em_gss_other :
26: em_gss_pro :
27: em_gss_rtd :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match				DB ID	Description
	Score	Length	DB	ID		
1	904	38.7	537	10	AW759200	AW759200 s138c06.Y
2	903	38.7	532	13	B1973838	B1973838 sa193d08.
3	868	37.2	650	12	BG524903	BG524903 8-8 Stev1
4	809	34.7	648	14	BQ852109	BQ852109 QGB17C13.
5	784	33.6	630	14	BQ855578	BQ855578 OGB27B05.
6	774	33.2	507	14	BM885973	BM885973 sam10d11.
7	744	31.9	673	10	BE322181	BE322181 NP010H12I
8	694	29.7	587	12	BG523648	BG523648 34-12 Ste
9	650	27.9	618	10	AV441327	AV441327 AV441327
10	624	26.7	635	12	BG522086	BG522086 18-18 Ste
11	614	26.3	596	12	BG525847	BG525847 54-55 Ste
12	590.5	25.3	724	12	BG127829	BG127829 EST473475
13	573	24.6	616	12	BG526525	BG526525 60-13 Ste
14	561	24.0	537	10	BE355801	BE355801 DGL_11_E0
15	560.5	24.0	527	14	BQ864610	BQ864610 QGC27C22.
16	543	23.3	593	17	BH777228	BH777228 f2mb013f0
17	518	22.2	1350	11	AK004914	AK004914 Mus muscu
18	510.5	21.9	529	10	AV442635	AV442635 AV442635
19	509.5	21.8	600	10	AV827187	AV827187 AV827187
20	500	21.4	657	13	BJ256228	BJ256228 BJ256228
21	485	20.8	1141	13	BM453791	BM453791 AGENCOURT
22	444.5	19.1	977	14	BO711543	BO711543 AGENCOURT
23	426	18.3	673	13	BJ261764	BJ261764 BJ261764
24	424.5	18.2	731	13	BI406095	BI406095 154E01.Ma
25	420.5	18.0	682	14	BM770153	BM770153 K-EST0053
26	420.5	18.0	737	14	BM770144	BM770144 K-EST0053
27	420.5	18.0	940	9	AL524311	AL524311 AL524311
28	413	17.7	514	10	AV528103	AV528103 AV528103
29	412.5	17.7	993	12	BG829912	BG829912 602764318
30	410.5	17.6	676	17	BH578169	BH578169 BQGM259F
31	405	17.4	608	14	BM771194	BM771194 K-EST0055
32	405	17.4	662	14	BM771402	BM771402 K-EST0055
33	400	17.1	928	14	BQ707084	BQ707084 AGENCOURT
34	397.5	17.0	767	11	AV112503	AV112503 Zea mays
35	391	16.8	401	13	BI139236	BI139236 F127P01Y
36	386	16.5	582	14	BM771795	BM771795 K-EST0055
37	385	16.5	637	14	BQ459510	BQ459510 HA08003F
38	378.5	16.2	827	9	A1047852	A1047852 uc66e07.Y
39	376.5	16.1	944	13	BI330091	BI330091 602982195
40	373.5	16.0	419	10	AV816862	AV816862 AV816862
41	372.5	16.0	837	13	BI327594	BI327594 602979775
42	372	15.9	841	12	BF310537	BF310537 601895241
43	369	15.8	551	14	BM770078	BM770078 K-EST0053
44	362	15.5	570	14	BM771852	BM771852 K-EST0055
45	355	15.2	370	10	BE355900	BE355900 DGL_11_E0

ALIGNMENTS

RESULT 1	AW759200	527 bp	mRNA	linear	EST 03-DEC-2001
LOCUS	AW759200				
DEFINITION	Gm-cl027-3587 5' similar to TR-092M42 Q92M42 F17L21.28. ; mRNA				
ACCESSION	AW759200				
VERSION	AW759200.1				
KEYWORDS	EST.				
SOURCE	soybean.				
ORGANISM	Glycine max				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotys; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.					

REFERENCE 1 (bases 1 to 527)
 AUTHORS Shoemaker, R., Keim, P., Vodka, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1800
 Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 for further information call: (800)-533-4363 or contact via email: ccu@resgen.com
 Insert Length: 900 Std Error: 0.00
 High quality sequence stop: 435.

FEATURES
 source
 1..527
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl027-3587"
 /clone_1b="Gm-cl027"
 /tissue_type="cotyledons of 3- and 7-day-old Williams seedlings"
 /lab_host="DH10B"
 /note="Vector: Bluescript II SK+; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (V-A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGACTCTCGAG(T)18] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GIBCOBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript(tm) II XR Predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene. 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."

BASE COUNT 156 a 107 c 116 g 148 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,91e-102 Length: 527
 Score: 904.00 Matches: 170
 Percent Similarity: 98.29% Conservative: 2
 Best Local Similarity: 97.14% Mismatches: 3
 Query Match: 38.75% Indels: 0
 DB: 10 Gaps: 0
 US-09-857-612a-14 (1-443) x AW759200 (1-527)

QY 210 SerHisSerLeuGlyGlyLeuPheValLeuGlnLeuLeuAsnArgAsnProProSerThr 229
 |||||
 Db 3 TCCACACTTTAGGAGGCGCTATTGTCTCTACACTACTAATAAGAACCCCGCTTGG 62
 QY 230 ArgLysLysPheIleLysHisPheIleAlaLeuSerAlaProTTPGlyGlyAlaIleAsp 249
 |||||
 Db 63 CGCAAAAATTCATCAAAACACTTATGCTCTTTCAGTCATGCGGGGGGCTATAGAC 122
 QY 250 GluMetTyrThrPheAlaSerGlyAsnThrLeuGlyValProLeuValAspProLeuLeu 269
 |||||
 Db 123 GAATGTACACCTTGGCATCTGCGACACCTTTGGAGTGGCCCTAGTGGACCTTTATTA 182
 QY 270 ValArgAspGlnArgSerSerGluSerAsnLeuThrLeuLeuProAsnProLysIle 289
 |||||
 Db 183 GTGAGGATGAAACAAGAACGCTCGAGATACCTTTGGCTTTGGCTTAACCAAAATTT 242
 QY 290 PheGlyProGlnLysProIleValIleThrProIleArgProTyrSerAlaHisAspMet 309
 |||||
 Db 243 TTTGGTCTCAAAAACCAATATGTATTAATCAATATGACCTATTCAGCTCATGACATG 302
 QY 310 ValAspPheLeuLysAspIleGlyPheProGlnGlyValTyrProTyrGluThrArgIle 329
 |||||
 Db 303 GTTGATTTTCTTAAAGACATTTGTTCTCTAAGGCGTTTATCTTATGAACACGAAAT 362
 QY 330 LeuProLeuIleGlyAsnIleLysAlaProGlnValProIleThrCysIleMetGlyThr 349
 |||||
 Db 363 CTACCTTGATAGGAGACATTAAGACACACACAGCTGCTTATTAATCTGATATATGGAACG 422
 QY 350 GlyValGlyThrLeuGlnThrLeuPheTyrGlyLysGlyAspPheAspGlnArgProGlu 369
 |||||
 Db 423 GGAATGGGAACCTTGGAACATTTGTTATATGGAAGGTGATTTTGATGAACGGCCAGAA 482
 QY 370 IleSerTyrGlyAspGlyAspGlyThrValAsnLeuValSerLeu 384
 |||||
 Db 483 ATATCATATGGGATGATGATGATGACGCTGATCTTGACTTG 527
 RESULT 2
 B1973838 532 bp mRNA linear EST 30-NOV-2001
 LOCUS sa193408.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
 DEFINITION ID: Gm-cl065-8607 5' similar to TR:092M42 Q92M42 F1L21.28. ; mRNA
 sequence.
 ACCESSION B1973838
 VERSION B1973838.1 GI:16348243
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids I: Fabales: Fabaceae: Papilionoideae: Phaseoleae; Glycine.
 REFERENCE 1 (bases 1 to 532)
 AUTHORS Shoemaker, R., Keim, P., Vodka, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1800
 Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 for further information call: (800)-533-4363 or contact via email: ccu@resgen.com
 High quality sequence stop: 421.
 Location/Qualifiers

FEATURES

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source
1. .532
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-8607"
/clone_lib="Gm-cl065"
/tissue_type="germinating shoots"
/lab_host="DH10B"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI. The cDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Williams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."
```

BASE COUNT 168 a 87 c 124 g 152 t 1 others

ORIGIN

Alignment Scores:

Pred. No.:	6,65e-102	Length:	532
Score:	903.00	Matches:	174
Percent Similarity:	98.87%	Conservative:	1
Best Local Similarity:	98.31%	Mismatches:	2
Query Match:	38.71%	Indels:	0
DB:	13	Gaps:	0

US-09-857-612A-14 (1-443) x BI973838 (1-532)

OY 254 PheAlaSerGlyAsnThrLeuGlyValProLeuValAspProLeuLeuValArgAspGlu 273
|||||
DB 2 TTTGCATCTGGCAACCTTTGGAGAGCCCTGTAGACCCCTTATTAGGAGGATGAA 61
OY 274 GlnArgSerSerGluSerAsnLeuTrpLeuLeuProAsnProValIlePheGlyProGln 293
|||||
DB 62 CAAAGAGCTCCGAGAGTAACTTTGGCTTTGCTTACCCCAAAATTTTGGTCTCCAA 121
OY 294 LysProIleValIleThrProIleArgProTyrSerAlaHisAspMetValAspPheLeu 313
|||||
DB 122 AAACCAATAGTGATATCTCAATAGACCTATTGACGCTATGACATGCTGATTTTCTA 161
OY 314 LysAspIleGlyPheProGluGlyValTyrProTyrGluThrArgIleLeuProLeuIle 333
|||||
DB 182 AAAGACATTGGTTTCTGAGGGGTTTATCTTATGAAACAGAAATTCATCCCTGATA 241
OY 334 GlyAsnIleLysAlaProGlnValProIleThrCysIleMetGlyThrGlyValGlyThr 353
|||||
DB 242 GGGACATTAAGACACCAAGTGCCTATTAAGTGTATGGAAGGGAGTGGGAACC 301
OY 354 LeuGluThrLeuPheTyrGlyGlyAspPheAspGluArgProGluIleSerTyrGly 373
|||||
DB 302 TTGGAACAATGTTTATGGGAAGTGATTTGATGAAAGCCGCAAGAAATATCNTATGGG 361
OY 374 AspGlyAspGlyThrValAsnLeuValSerLeuLeuAlaLeuGlnSerLeuTrpLysGlu 393
|||||
DB 362 GAGGTGATGAGGAACGGTGAACCTGTGAGCTTGTGGCCCTCAATCACTATGAAAGAG 421
OY 394 GluLysAspGlnTyrLeuLysValIleLysIleAspGlyValSerHisThrSerIleLeu 413
|||||
DB 422 GAGAAATAATCAATACCTTAAGTGGTTAAGATGATGGGTGCTCTCACTACTCAAAACTT 461
OY 414 LysAspGluValAlaLeuAsnGluIleValGlyGluIleThrSerIleAsn 430
|||||
DB 482 AAGGATGAGAGTTGCACTAAATGAAATAGTAGTGAGATTCACTCAATTTAT 532

RESULT 3
BG524903 650 bp mRNA linear EST 16-NOV-2001
LOCUS

DEFINITION 8-8 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA sequence.
ACCESSION BG524903
VERSION BG524903.1 GI:16948350
KEYWORDS EST.
SOURCE Stevia rebaudiana.
ORGANISM Stevia rebaudiana
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids II: Asterales: Asteraceae: Asteroideae; Helianthaceae; Stevia.
1 (bases 1 to 650)
REFERENCE
AUTHORS Brandle, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.
TITLE Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in diterpene synthesis
JOURNAL Unpublished (2001)
COMMENT Contact: Jim Brandle
Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCPPRC
1391 Sandford St., London, Ontario, CANADA, N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: brandleje@am.agr.ca
Seq primer: T3 promoter primer.
Location/Qualifiers
1. .650
/organism="Stevia rebaudiana"
/strain="751/1501"
/cultivar="Landrace"
/db_xref="taxon:55670"
/clone_lib="Stevia field grown leaf cDNA"
/tissue_type="leaf"
/dev_stage="field grown, mid-size"
/lab_host="E. coli strain XL0LR"
/notes="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI. This cDNA library was constructed from polyA+ enriched mRNA from field grown leaves. Mid-size actively growing leaves were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The cDNA was prepared using an XhoI-poly(dT) linker-primer. An EcoRI adapter was ligated to the blunt end cDNA and the products were digested with EcoRI and XhoI enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the host strain XL1-Blue MRF. Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XL0LR. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTACCTCACTAAAGGGA 3'. This library was constructed by Alex Richman."

BASE COUNT 171 a 164 c 143 g 171 t 1 others

ORIGIN

Alignment Scores:

Pred. No.:	2.18e-97	Length:	650
Score:	868.00	Matches:	160
Percent Similarity:	85.58%	Conservative:	24
Best Local Similarity:	74.42%	Mismatches:	31
Query Match:	37.21%	Indels:	0
DB:	12	Gaps:	0

US-09-857-612A-14 (1-443) x BG524903 (1-650)

OY 79 PheArgLeuTrpPheAspSerValIleLeuAlaProPheThrGlnCysPheAlaGlu 98
|||||
DB 1 TTCAGGCTATGGTTCGAGGCGCGGTGTGTGGCACCGGTGACCGAGTGTGGCCGAT 60
OY 99 ArgMetThrLeuHisTyrHisGlnGluLeuAspAspTyrPheAsnThrProGlyValGlu 118
|||||
DB 61 CGTATGCGCTTACTATGACCGAGATGCGATGATACAAAATAGTCCGCGAGTGGAG 120
OY 119 ThrArgValProHisPheGlySerThrAsnSerLeuLeuTyrLeuAsnProArgLeuLys 138
|||||
DB 121 ACTAGAGTGTCTGAGTTGTGCTTACTACATCCCTCTCTACCTTGATCGATCTTCAAG 180

FEATURES	source
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
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SOURCE	
ORGANISM	
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BASE COUNT	167 a	153 c	168 g	160 t
ORIGIN	TAG_LIB-06_ABCDI lettuce salinas TAG_TISSUE-chemical induction TAG_SEQ-TGAGCCGCG			
Alignment Scores:				
Pred. No.:	5.03e-90	Length:	648	
Score:	809.00	Matches:	149	
Percent Similarity:	83.80%	Conservative:	32	
Best Local Similarity:	68.98%	Mismatches:	35	
Query Match:	34.68%	Indels:	0	
DB:	14	Gaps:	0	
US-09-857-612A-12 (1-443) x B0852109 (1-648)				
QY	177	glyhspProSerGlnValGlySerlyPheLeuLysAspPheLysAsnLeuIleGlu	196	
Db	1	GGGCATCCCTTGGCGAGTGGCTCCACCTTCCTCCAAACATTAACAGTTATATCAGGAA	60	
QY	197	AlaserAsnSerAsnAsnglyLysProValIleLeuLeuSerHisSerLeuLysGlyLeu	216	
Db	61	GCAAGGATTCAAAGGTGGAAACCCGTCATTCATCTCCCATAGTCTCGTGCCCTC	120	
QY	217	PheValLeuGlnLeuLeuAsnArgAsnPropProSerTParGlyLysPheIleLysHis	236	
Db	121	TTTCGCTCTCCACTCTCTCAACCGCAACCCAGCTCTCGGGAACATATCATTAAGCAC	180	
QY	237	PheIleAlaLeuSerAlaProTrrpGlyAlaIleAspGluMetYrrThrPheAlaser	256	
Db	181	TTTCATCGCACTAGCGGACCATGGGATGGCAGGTTGACAGAGATGTTCACCTTTGCATTC	240	
QY	257	GlyAsnThrLeuGlyValProLeuValAspProLeuLeuValArgAspGluGlnArgSer	276	
Db	241	GGGAATTCACTAGAGAGTCCCTCGTAAACCCCTTGGCTTTGATGAAGAACCAACGAGAC	300	
QY	277	SerGluSerAsnLeuTrrpLeuLeuProAsnProLysIlePheGlyProGlnLysProIle	296	
Db	301	TCAGAGAGCACTTATGGCTATTTGCCAGGTACAAACGATTTCCCGCAGAGAAACCACTT	360	
QY	297	ValIleThrProIleArgProTrrySerAlaHisAspMetValAspPheLeuLysAspIle	316	
Db	361	GTTGTTACCAAAAACCTGCATATCTCTTGTATATTTCMAAGATTTTACAGATATTC	420	
QY	317	GlyPheProGluGlyValTrrProGlyGluThrArgIleLeuProLeuIleGlyAsnIle	336	
Db	421	GCGCTTCTCGAAGGGGTGCAGCCCTTACCAAGAACCCGCTTCCTTGGTGAGAGATTG	480	
QY	337	LysAlaProGlnValProIleThrCysIleMetGlyThrGlyValGlyThrLeuLunThr	356	
Db	481	GCTGCACCAAGCAATTCGGTAACATGTATTATCGGAAGTGCAGTTCAACACCGCGAATCT	540	
QY	357	LeuPheTrrGlyLysGlyAspPheAspGluArgProGluIleSerTrryGlyAspIlyAsp	376	
Db	541	TTTGCAATTACGGGAAGAGGGGTTGATTAAGCAGCCGGAGATTGTGTACGGAGATGAGAT	600	
QY	377	GlyThrValAsnLeuValSerLeuLeuAlaLeuGlnSerLeuTrrPlys	392	
Db	601	GGGACGCGTAACATGGCGAGCTTGTGGCTTTGGTGAGATGAGTGGAGG	648	

RESULT 5

LOCUS B0855578

DEFINITION OG227805.yg.ab1 OG_ABCDI lettuce salinas lactuca sativa cDNA clone

630 bp

mRNA

linear

EST 14-AUG-2002

QGB27B05, mRNA sequence.
 BO855578
 VERSION BO855578.1 GI:22241043
 KEYWORDS EST.
 SOURCE Lactuca sativa.
 ORGANISM Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eusterids II; Asterales; Asteraceae; Lactuceae; Lactuca

REFERENCE 1 (bases 1 to 630)
 AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolkmann, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
 TITLE Lettuce and Sunflower ESTs from the Composite Genome Project
 JOURNAL http://compgenomics.ucdavis.edu/
 COMMENT Unpublished (2002)
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@catc.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig QG_CA.Contig973, see http://cgpbdb.ucdavis.edu/ for details.
 Plate: QGB27 row: B column: 05.

FEATURES
 source
 Location/Qualifiers
 1..630
 /organism="Lactuca sativa"
 /cultivar="Salinas"
 /db_xref="taxon:4236"
 /clone="QGB27B05"
 /clone_1id="QG_ABCDI lettuce salinas"
 /lab_host="E.coli"
 /note="Vector: pBRCDNA5fiAB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpbdb.ucdavis.edu/
 TAG_LIB=QG_ABCDI lettuce salinas
 TAG_TISSUE=chemical induction
 TAG_SEQ=TAGCGCGG"

BASE COUNT 166 a 153 c 157 g 154 t
 ORIGIN

Alignment Scores:
 Pred. No.: 6,35e-87 Length: 630
 Score: 784.00 Matches: 145
 Percent Similarity: 83.81% Conservative: 31
 Best Local Similarity: 69.05% Mismatches: 34
 Query Match: 33,608 Indels: 0
 Db: 14 Gaps: 0

US-09-857-612a-14 (1-443) x BO855578 (1-630)

QY 177 GYHISProSerGIInValIGYSerLYSPhelLeuLYSAspLeuLYSAsnLeuILEGlu 196
 Db 1 GGGCATCTTGGCGACGCGGCTCCACCTCTCCAAACATTAACGTTAATCGAGGAA 60

QY 197 ALASerASnSerASnAnGlyLYSProVALILEuLeuSerHisSerLeuGLYGLYLeu 216
 Db 61 GCAAGGATTCATCAATGGTGGAAACCGCATCTCTATCTCCATATCTCGGGGCTC 120

QY 217 PhVaILLeuGLILEuLeuASnArGAsnProProSerTrpArGLYLYSPhelLeuLYS 236
 Db 121 TTGCTCTCCACTCTCAACCGCAACCCACGCTCTCGGCGAAACATATCAATAAACGAC 180

QY 237 PheILLeuASerAlaProTrpGLYGLYAlaILEAspGLuMetYrThrPheAlaSer 256
 Db 181 TTGATCGCAGGAGGGGACCATGGGGGCGACGGTTACAGAGTGTGACTTTGCATGCC 240

QY 257 GLYASnThrLeuGLYGLYAlaProLeuValAspProLeuLeuValArgAspGLuGLnArgSer 276
 Db 241 GGGAAATTCACATGAGAGGCCCTCCCTGTAACCCCTTGCTGTGTAGAAACGAACACGAGC 300

QY 277 SerGIuSerSnLeuTrpPheLeuProAsnProLYSILEPheGLYProGLnProILE 296
 Db 301 TCAGAGACCACTTATGGCTATTGTCACATCAAGACAGTTCGCCGAGAGAACCACTT 360

QY 297 ValILEThrProILEArGProTYrSerAlaHisAspMetValAspPheLeuLYSAspILE 316
 Db 361 GTTGTTCACAAACACCTGCAGCTATTCTTCTTTGATATTTCACATTTTGAAGATATC 420

QY 317 GLYPheProGLuGLYAlaTYrProTYrGLuThrArgILELeuProLeuILEGLYAsnILE 336
 Db 421 GGCTTCTCTGAAGGGGTGACGCTTACAGAAACGCGCTTGCCCTGGTGAAGAAAGTTG 480

QY 337 LysAlaProGLnValProILEThrCYsILEMetGLYThrArgYAlaGLYThrLeuGLuThr 356
 Db 481 GCTGACCAAGAAATTCGCTAATGATGTAATGGAAGTGGAGTCAAGACCGGAAATCT 540

QY 357 LeuPheTYrGLYLYSGLYAspPheAspGLuArgProGLuILESerTYrGLYAspGLYAsp 376
 Db 541 TTGCATTACGAGAGAAACGGTTTGATGATACGACCGGAGATTTGCTACGAGATGGAGAT 600

QY 377 GLYThrValAsnLeuValSerLeuLeuAla 386
 Db 601 GGCACGGTGAAATGCGGAGCTGTGGCT 630

RESULT 6
 LOCUS BO855973
 DEFINITION semi0d11.y1 Gm-cl063 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-cl063-5158 5' similar to TR:Q9ZM42 Q9ZM42 F17L21.28. ;, mRNA sequence.

ACCESSION BO855973
 VERSION BO855973.1 GI:19269717
 KEYWORDS soybean.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eudrosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 507)
 AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvelli, V., Rhana, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 TITLE Public soybean EST project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R./Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com
 Seq primer: -40RP from Glibco
 High quality sequence stop: 421.
 Location/Qualifiers
 1..507
 /organism="Glycine max"
 /db_xref="taxon:3847"

FEATURES
 source

/clone="SOYBEAN CLONE ID: Gm-cl063-5158"
 /clone_lib="Gm-cl063"
 /tissue_type="Germinating shoot, 24 hour germination"
 /lab_host="DH10B"
 /note="Vector: pBluescript II SK+, Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to harvesting the germinating shoots. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."

BASE COUNT 145 a 125 c 100 g 137 t

ORIGIN

Alignment Scores:

Pred. No.: 7,83e-86 Length: 507
 Score: 774.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 33.18% Indels: 0
 DB: 14 Gaps: 0

US-09-857-612a-14 (1-443) x BM855973 (1-507)

QY 1 MetLysLysGluGluGluGluGluLysIleGluValAlaThrLeuThrValThrVal 20
 DB ATGAAGAAGAAAGAAAGAGAGGCTCTCAAGATTGAGTTGACACCTCAGATTACAGTA 135
 QY 21 ValValValMetLeuSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
 DB GTTGTCTTGATGCTGCTCATTTCTATGACATGCGGACCAACCTGACCTTTGATT 195
 QY 136 GTTGTCTTGATGCTGCTCATTTCTATGACATGCGGACCAACCTGACCTTTGATT 195
 QY 41 LeuLeuProGluAsnGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
 DB CTTATACAGAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 255
 QY 196 CTTATACAGAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 255
 QY 61 SerThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
 DB TCTACTTTCATCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 315
 QY 256 TCTACTTTCATCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 315
 QY 81 LeuTrpPheAspSerSerValIleLeuAlaProPheThrGlnCysPheAlaGluArgMet 100
 DB CTTGGTTTGAATCCAGTGTCTATGCTCTCTTCACTCAATGCTTGGCCGAAGCATG 375
 QY 316 CTTGGTTTGAATCCAGTGTCTATGCTCTCTTCACTCAATGCTTGGCCGAAGCATG 375
 QY 101 ThrLeuHisTrpHisGlnGluLeuAspAspTrpPheAsnTrpProGluValGluThrArg 120
 DB ACCCTTATATCCACCAAGAACTCGATGATTAATCTTCAACACTCCCTGGGGTTGAGACCCGG 435
 QY 376 ACCCTTATATCCACCAAGAACTCGATGATTAATCTTCAACACTCCCTGGGGTTGAGACCCGG 435
 QY 121 ValProHisPheGlySerThrAsnSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 140
 DB GTCCCTCACTTGGTTCACCACTCTCTCTATCTCATCTCCGCTCAAGCATATC 495
 QY 436 GTCCCTCACTTGGTTCACCACTCTCTCTATCTCATCTCCGCTCAAGCATATC 495
 QY 141 ThrGlyTrpMet 144
 DB TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 144
 QY 496 ACCGATACATG 507

RESULT 7
 BE322181
 LOCUS BE322181 673 bp mRNA linear EST 14-JUL-2000
 DEFINITION NF010H12IN1101 Insect herbivory Medicago truncatula cDNA clone
 ACCESSION BE322181
 VERSION BE322181.1 GI:9195958
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 CONTACT: KORTH K
 DEPT. OF PLANT PATHOLOGY
 UNIVERSITY OF ARKANSAS
 217 PLANT SCIENCE BUILDING, FAYETTEVILLE, AR 72701, USA
 TEL: 501 575 5191
 FAX: 501 575 7601
 EMAIL: KORTHCOMP@ARK.EDU
 MEDICAGO GENOME INITIATIVE accession: MGI:S:24007
 INSERT LENGTH: 673 Std Error: 0.00
 PLATE: 010 row: H column: 12
 Seq primer: TCACACAGGAACAGCATATGAC.

FEATURES

source

Location/Qualifiers
 1..673
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone_lib="NF010H12IN"
 /clone_lib="Insect herbivory"
 /tissue_type="local and systemic leaves"
 /dev_stage="mature"
 /note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

BASE COUNT 207 a 143 c 110 g 213 t

ORIGIN

Alignment Scores:

Pred. No.: 6.99e-82 Length: 673
 Score: 744.00 Matches: 146
 Percent Similarity: 84.24% Conservative: 25
 Best Local Similarity: 71.92% Mismatches: 22
 Query Match: 31.89% Indels: 10
 DB: 10 Gaps: 3

US-09-857-612a-14 (1-443) x BE322181 (1-673)

QY 5 GlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 24
 DB TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 24
 QY 70 AAGGAACATAGCTCAAAATTTGCAATT--ACCAATACATGAGACA--CTGTTAGTAATG 123
 QY 25 LeuSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 38
 DB GTATGCTTAATTTGTTGGACAAATGTTCCGTTGATACACCAACCAACCTCAATCA 183
 QY 124 GTATGCTTAATTTGTTGGACAAATGTTCCGTTGATACACCAACCAACCTCAATCA 183
 QY 39 LeuLeuLeuLeuProGluAsnGluGluGluGluGluGluGluGluGluGluGluGlu 58
 DB GTGATTAATAATACCAAGTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 243
 QY 184 GTGATTAATAATACCAAGTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 243
 QY 59 LysProSerThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 78
 DB AAACCTTCTACCTTAATTTGATGATCCATGATCCCTCTTCAAGAAAGAAAGGCTCG 303
 QY 244 AAACCTTCTACCTTAATTTGATGATCCATGATCCCTCTTCAAGAAAGAAAGGCTCG 303
 QY 79 PheArgLeuTrpPheAspSerSerValIleLeuAlaProPheThrGlnCysPheAlaGlu 98
 DB TTTTGAATTAATGCTTGAATTAATGCTTGAATTAATGCTTGAATTAATGCTTGAATTA 363
 QY 304 TTTTGAATTAATGCTTGAATTAATGCTTGAATTAATGCTTGAATTAATGCTTGAATTA 363
 QY 99 ArgMetThrLeuHisTrpHisGlnGluLeuAspAspTrpPheAsnTrpProGluValGlu 118
 DB CGCATGACTCTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
 QY 364 CGCATGACTCTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
 QY 119 ThrArgValProHisPheGlySerThrAsnSerLeuLeuLeuLeuLeuLeuLeuLeu 138
 DB TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 138

Db 424 ACAAGTCCCTAGCTTTGGTCTACTTCCTCTCTTATCTTAATCCTGCTTAAAG 483
 Oy 139 HSL1eThrGlyTyrMetAlaProLeuValAspSerLeuGlnLysLeuGlyTyrAlaAsp 158
 Db 484 CTTGTACACAGGCTACATGGCCCTTAGTATGATCATATGACACAGCTGGTTCATATAG 543
 Oy 159 GlyGluThrLeuPheGlyAlaProTyrAspPheArgTyrGlyLeuAlaGlnGlyHis 178
 Db 544 GGTCAAAATCTGTTGGAGCTCCCTATGATTTTCGATATGCTAGACAGCACCAAGTCAC 603
 Oy 179 ProSerGlnVal-GlySerLysPheLeuLysAspLeuLysAsn-LeuIleGlnGluAla 198
 Db 604 CCATTCAGATGGTGGTCCAAATTCCTAAGACCTAAAGAAATTTGATGAGAAAGCAA 663
 Oy 198 erasn 199
 Db 664 GCAC 668
 RESULT 8
 BG523648
 LOCUS 587 bp mRNA linear EST J6-NOV-2001
 DEFINITION 34-12 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
 sequence.
 ACCESSION BG523648
 VERSION BG523648.1 GI:16947068
 KEYWORDS EST.
 SOURCE Stevia rebaudiana.
 ORGANISM Stevia rebaudiana.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; easterids II; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Stevia.
 1 (bases 1 to 587)
 Brandle, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.
 Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in
 diterpene synthesis
 Unpublished (2001)
 Contact: Jim Brandle
 Genomics and Biotechnology
 Agriculture and Agri-Food Canada - SCFRC
 1391 Sandford St., London, Ontario, CANADA, N5V 4T3
 Tel: 519 457 1470
 Fax: 519 457 3997
 Email: brandleje@agr.ca
 Seq primer: T3 promoter primer.
 Location/Qualifiers
 1..587
 /organism="Stevia rebaudiana"
 /strain="751/1501"
 /cultivar="Landrace"
 /db_xref="taxon:55670"
 /clone_lib="Stevia field grown leaf cDNA"
 /tissue_type="leaf"
 /dev_stage="field grown, mid-size"
 /lab_host="E. coli strain XL0LR"
 /note="Vector: pBK-CMV; Site.1: EcoRI; Site.2: XhoI; This
 cDNA library was constructed from polyA+ enriched mRNA
 from field grown leaves. Mid-size actively growing leaves
 were collected and pooled from several plants and frozen
 immediately after harvesting in liquid nitrogen. The cDNA
 was prepared using an XhoI-poly(dT) linker-primer. An
 EcoRI adapter was ligated to the blunt end cDNA and the
 products were digested with EcoRI and XhoI enabling
 directional cloning into the lambda ZAP Express vector.
 The library was amplified using the host strain XL1-Blue
 MRF'. Mass excision of the library was performed to
 obtain pBK-CMV phagemid clones in the host strain XL0LR.
 Single pass DNA sequencing was performed using the T3
 promoter primer: 5' ATTAACCTCACTAAAGCA 3'. This library
 was constructed by Alex Richman."
 BASE COUNT 161 a 112 c 155 g 158 t
 ORIGIN

Alignment Scores:
 Pred. No.: 9, 72e-76 Length: 587
 Score: 694.00 Matches: 132
 Percent Similarity: 82.29% Conservative: 26
 Best Local Similarity: 68.75% Mismatches: 33
 Query Match: 29.75% Indels: 1
 DB: 12 Gaps: 0
 US-09-857-612A-14 (1-443) x BG523648 (1-587)
 Oy 224 ArgAsnProSerThrPArgLysPheLysHisPheIleAlaLeuSerAlaPro 243
 Db 3 CGTAACCCACCCCTCATGCGCCCAACAAATACATTAATTAATTCGGTTCGCGACCA 62
 Oy 244 ThrGlyGlyAlaIleAspGlnMetTyrThrPheAlaSerGlyAsnThrLeuGlyValPro 263
 Db 63 TGGGTGTGAACGGTTGACGAGATGTTTACCTTTGCTCTGGAGACACTGTGGAGTTCCA 122
 Oy 264 LeuValAspProLeuLeuValArgAspGlnArgSerSerGlnSerAsnLeuTyrLeu 283
 Db 123 CTGGTGAACCCGTTGCTGTCAGAGAAATGACAAACGAGTTCTGAAACCAFTTATGGCTC 182
 Oy 284 LeuProAsnProLysIlePheGlyProGlnLysProIleValIleThrProIleArgPro 303
 Db 183 ATGCCACGACGAAACAAATTCCTCAACAGACACTGTAGTGTGCATCAGATTCAACT 242
 Oy 304 TyrSerAlaHisAspMetValAspPheLeuLysAspIleGlyPheProGlnGlyValTyr 323
 Db 243 TACTCGCTTTTGAACATTCACGGTTTCTTAAGATATCGGGTTCGAGAGGGGTGTCCAC 302
 Oy 324 ProTyrGlnThrArgIleLeuProLeuIleGlyAsnIleLysAlaProGlnValProIle 343
 Db 303 CCTTACGACAGACAGCAATCTTGCTGCTTGGTGAAGATTGGTTGACCGGGAGTCCCGCTA 362
 Oy 344 ThrCysIleMetGlyThrGlyAlaGlyThrLeuGlnThrLeuPheTyrGlyLysGlyAsp 363
 Db 363 ACGGTATAGTTGGAACGCGAATGTTATGAGATGTCAGCAACGGTAACCTTGTATATGGGACGACGGG 422
 Oy 364 PheAspGlnArgProGlnIleSerTyrGlyAspGlyAspGlyThrValAsnLeuValSer 383
 Db 423 TTGCATAGACGACCGGAATGTTATGAGATGTCAGCAACGGTAACCTTGTATATGGGACGACGGG 482
 Oy 384 LeuLeuAla-LeuGlnSerLeuTyrPlyGlnLysAsnGlnTyrLeuLysValValLys 403
 Db 483 TTGTGGCTTTTGGACAGACAGTCGAGATGAAAGATCAGCAATTTGAAGGAGATTAA 542
 Oy 403 sIleAspGlyValSerHisThrSerIleLeuLys 414
 Db 543 GCTTACNGGATTTTCATACAGACATCACTTAA 576
 RESULT 9
 AV441327/c 618 bp mRNA linear EST 14-NOV-2000
 LOCUS AV441327 Arabidopsis thaliana above-ground organ two to six-week
 DEFINITION old Arabidopsis thaliana cDNA clone AB242902_f 3', mRNA sequence.
 ACCESSION AV441327
 VERSION AV441327.1 GI:7611713
 KEYWORDS EST.
 SOURCE chalc cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 618)
 Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 A large scale analysis of cDNA in Arabidopsis thaliana: Generation
 of 12,028 non-redundant expressed sequence tags from normalized and
 size-selected cDNA libraries
 DNA Res. 7, 175-180 (2000)
 JOURNAL 20363093
 MEDLINE Contact: Erika Asamizu
 COMMENT The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizuekazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
 Location/Qualifiers

FEATURES

source

1..618
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone_id="AP242902.f"
 /clone_lib="Arabidopsis thaliana above-ground organ two to six-week old"
 /tissue_type="aboveground organs"
 /dev_stage="two to six-week old"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 163 a 155 c 125 g 175 t
 ORIGIN

Alignment Scores:

Pred. No.: 3.3e-70 Length: 618
 Score: 650.00 Matches: 127
 Percent Similarity: 75.49% Conservative: 27
 Best Local Similarity: 62.25% Mismatches: 42
 Query Match: 27.86% Indels: 8
 DB: 10 Gaps: 2

US-09-857-612a-14 (1-443) x AV441327 (1-618)

QY 228 seTTPaTgLySPhneLlYsHlSpheLleAlaLeuSerAlaProTgPlyGlyAla 247

DB 618 TCATGGCGCCGAGTACATCAACACTTGTTCACACGCTGCCCATGGGCGGAGC 559

QY 248 lLaSpGluMeTyrTrhPheAlaSerGlyAsnThrLeuGlyValProLeuValAspPro 267

DB 558 ATCTCTCAGATGAGACATTTGCTTCTGGCAACACACTCGGTGCTTCTTGTAGTTAACCT 499

QY 268 LeuLeuValArgAspGluArgSerSerGluSerAsnLeuTrpLeuLeuProAsnPro 287

DB 498 TTGGTGGTCACAGCGCATCAGAGACCTCCGAGAGTACCAATGGCTCTTCATCTAC 439

QY 288 LySAllePheGlyProGln--LysProIleValIleThrProIleArgProTyrSerAla 306

DB 438 AAAGTCTTTCACAGACAGAACACTAACCGCTTCCGAACTCCCGACGTTAACTACACACT 379

QY 307 HlAspMeTValAspPheLeuLysAspIleGlyPheProGluGlyValTyrProTyrGlu 326

DB 378 TACGAGATGATCGGTTTGTTCAGACATTCGATTGTCACAAGAGTGTGCTTACAAAG 319

QY 327 ThrArgIleLeuProLeuIleGlyAsnIleLysAlaProGlnValProIleThrCysIle 346

DB 318 ACAAGAGTGTGCTTTCACAGACAGAGCTGATGACTCCGGAGTCCAGTCACTTGCACTA 259

QY 347 MetGlyThrGlyValGlyThrLeuGluThrLeuPheTyrGlyGlyAspPheAspGlu 366

DB 258 TATGGGAGAGAGAGTTCATACACCGAGGTTTGTATGTGAAAAAGAGATTCATAG 199

QY 367 ArgProGluIleSerTyrGlyAspGlyAspGlyThrValAsnLeuValSerLeuLeuAla 386

DB 198 CAACAGAGATTAAGTATGAGATGAGATGAGAGCGGTTAATTGGCAGCTTACACT 139

QY 387 LeuGlnSerLeuTrpLysGluGlyAsnGlnTyrIleLeuLysValValIleAspGly 406

DB 138 TTG-----AAAGTCATAGCTTGAACACCGTGAAGATGATGAGA 100

QY 407 ValSerHlSerIleLeuLysAspGlyValAlaLeuAsnGlnIleValGlyGluIle 426

DB 99 GTTTCGCGATCATATCACTTAAGACGAGATCCGACTTAAGAGATTATGACAGATT 40

QY 427 ThrSerIleAsn 430

DB 39 TCATATTATTAT 28

RESULT 10

BG522086

LOCUS BG522086 635 bp mRNA linear EST 01-FEB-2002

DEFINITION 18-18 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA sequence.

ACCESSION BG522086

VERSION BG522086.1 GI:18465150

KEYWORDS EST.

SOURCE Stevia rebaudiana.

ORGANISM Stevia rebaudiana

REFERENCE 1 (bases 1 to 635)

AUTHORS Brandt, D.E., Richman, A., Swanson, A.K. and Chapman, B.P.

TITLE Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in dipterene synthesis

JOURNAL Unpublished (2001)

COMMENT Contact: Jim Brandt

Genomics and Biotechnology

Agriculture and Agri-Food Canada - SCPPRC

1391 Sandford St., London, Ontario, CANADA, N5V 4T3

Tel: 519 457 1470

Fax: 519 457 3997

Email: brandtje@em.agr.ca

Seq primer: T3 promoter primer.

Location/Qualifiers

1..635

/organism="Stevia rebaudiana"

/strain="751/1501"

/cultivar="landrace"

/db_xref="taxon:55670"

/clone_id="Stevia field grown leaf cDNA"

/tissue_type="leaf"

/dev_stage="field grown, mid-size"

/lab_host="E. coli strain XL0R"

/note="Vector: pbk-CMV. Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from polyA+ enriched mRNA from field grown leaves. Mid-size actively growing leaves were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The cDNA was prepared using an XhoI-poly(dT) linker-primer. An EcoRI adapter was ligated to the blunt end cDNA and the products were digested with EcoRI and XhoI enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the host strain XL1-Blue MRF+. Mass excision of the library was performed to obtain pbk-CMV phagemid clones in the host strain XL0R. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTACCTCCTCAAGGCA 3'. This library was constructed by Alex Richman."

BASE COUNT 158 a 157 c 164 g 155 t

ORIGIN

Alignment Scores:

Pred. No.: 6.08e-67 Length: 635

Score: 624.00 Matches: 121

Percent Similarity: 73.46% Conservative: 34

Best Local Similarity: 57.35% Mismatches: 44

Query Match: 26.75% Indels: 13

DB: 12 Gaps: 1

US-09-857-612a-14 (1-443) x BG522086 (1-635)

QY 11 lLeGluValAlaTrpThrValThrValValValMetLeuSerLeuLeuCysThr 30

DB 4 GTTCGGTTCAGCCAGATCAGATGCTATGCCACGATGCTGGGTTGCCACCATACACT 63

QY 31 CysGlyAlaSer-----AsnLeuAspPro 38

DB 64 TGTGGCGCAAGCATCATATACCATCACCACGACGACGAGAACCATCGGCTGATCCG 123

QY 39 LeuIleLeuIleProGlyAsnGlyAsnGlnLeuGlnAlaArgLeuThrAsnGlnTyr 58

```

Db      124 GTGATCTGGTGGCTGGAGCGGTGGGAACACAGTAGAACCCGGTTAACGCCGAGTAT 183
Qy      59 LysProSerThrphelecygsluserTPryProleuilelyslslysaanglytrp 78
      184 AAGGGGACATAGCTGGTGTGTCACACCGGTTCTACCCGCTCAAGAAAGATGAGGGGGGTGG 243
Qy      79 PheArgLeuThrpphelecygsserSerValIleLeuAlaProPheThrcIncySpheAlaGlu 98
      244 TTCAGGCTATGCTTCGAGAGTCGGCGTGTGTGGACCATGACCGAGTCTTTGGCCGAT 303
Db      99 ArgMetThrleuHsIstYrHisGInGluLeuAspAspTytrPheAsnThrProGlyValGlu 118
      304 CGTATGACCGTTTACTACTACCCAGATGTCGATGATTACAAATATGCTCCCGAGTGGAG 363
Qy      119 ThrArgValProHisPheGlySerThrAsnSerLeuLeuLeuLeuLeuAsnProAlaGlyLeu 138
      364 ACTAGAGTGTCTCAGTTGTGTCTTACTACTCAATCGCTTCTTCACTGATCTTTCTCAAG 423
Qy      139 HisIleThrGlyTyrMetAlaProLeuValAspSerLeuGlnIlysluGlyTyrAlaAsp 158
      424 CATATACACATACATACATGACACCATGTCGATCTATACACACACTGGCTCAAAAGAT 483
Qy      159 GlyGluThrLeuPheGlyAlaProTytrAspPheArgTytrGlyLeuAlaGluGlyHis 178
      484 ACCGAGAACTCTTTCGAGCTCATATGATTTTCGNTACGCGGTAGCATCCGAAAGCAT 543
Qy      179 ProSerGlnValGlySerlyspheleuLyAspLeuLyAsnLeuIleGluAlaSer 198
      544 CCTGTGATGTGCGGTCACTTACTCTCAAAACCTAAAGGATTAAACGAAAGCGAAGC 603
Qy      199 AsnSerAsnAsnGlyLysProValIleLeuLeu 209
      604 AC-ACAAATGGCGGACTCCCGGTGATCTCTGTC 635
Db      604 AC-ACAAATGGCGGACTCCCGGTGATCTCTGTC 635

RESULT 11
Bg525847      596 bp      mRNA      linear      EST 16-NOV-2001
LOCUS      54-55 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
DEFINITION      sequence.
ACCESSION      BG525847
VERSION      BG525847.1 GI:16949308
KEYWORDS      EST.
SOURCE      Stevia rebaudiana.
ORGANISM      Stevia rebaudiana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; easterids II; Asterales; Asteraceae; Asteroideae;
Heliantheae; Stevia.
1 (bases 1 to 596)
Brandle, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.
Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in
diterpene synthesis
Unpublished (2001)
Contact: Jim Brandle
Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCPPRC
1391 Sandford St., London, Ontario, CANADA, N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: brandleje@em.agr.ca
Seq primer: r3 promoter primer.
Location/Qualifiers
1..596
/organism="Stevia rebaudiana"
/strain="751/1501"
/cultivar="Landrace"
/db_xref="taxon:55670"
/clone.lib="Stevia field grown leaf cDNA"
/tissue_type="leaf"
/dev_stage="field grown, mid-size"
/lab_host="E. coli strain XL0R"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA

```

from field grown leaves. Mid-size actively growing leaves were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The cDNA was prepared using an XhoI-poly(dT) linker-primer. An EcoRI adapter was ligated to the blunt end cDNA and the products were digested with EcoRI and XhoI enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the host strain XL1-Blue MR⁺. Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XL0R. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTAACCTCACTAAAGGA 3'. This library was constructed by Alex Richman."

```

BASE COUNT      153 a      147 c      149 g      147 t
ORIGIN
Alignment Scores:
Pred. No.:      9.7e-66      Length:      596
Score:      614.00      Matches:      114
Percent Similarity:      73.74%      Conservative:      32
Best local Similarity:      57.58%      Mismatches:      40
Query Match:      26.32%      Gaps:      12
DB:      12      Gaps:      1

US-09-857-612A-14 (1-443) x BG525847 (1-596)
Qy      15 ThrleuThrValThrValValValMetleuSerleuCystrCyglyAlaSer 34
      3 ACGATACAGATGGCTATCGCACAGCATGTGGCGGTGACCCACCATACCTTGGCGGACAG 62
Db      35 -----AsnleuAspProleuIleleuIle 42
      63 ATCATATATACCATCACACACAGCCACAGACATCGGCTGTATCCGGTATCTGTG 122
Qy      43 ProGlyAsnGlyLyAsnGlnLeuGluAlaArgLeuThrAsnGlnTytrLysProSerThr 62
      123 CCTTGAGCCGCGGTGGAGACCATGTAAGCCCGGTAAAGCGCGATTAAGAGGAGATACG 182
Qy      63 PheIleCygsluserTPryProleuilelyslslysaanglytrppheArgLeuTrp 82
      183 TGGTTGTGCAACCGGTTCTACCCGCTCAAGAAAGATGAGGGGGGTGTCAGGCTATGG 242
Qy      83 PheAspSerSerValIleLeuAlaProPheThrcIncySpheAlaGluArgMetThrleu 102
      243 TTCAGAGTCGGCGTGTGTGGCACCATTCGACGAGTCTTTGCCGATCGATACGCTT 302
Qy      103 HisTytrHisGInGluLeuAspAspTytrPheAsnThrProGlyValGluThrArgValPro 122
      303 TACTATGACCGAGATGTCGATGATTACAAATATGCTCCCGAGGAGGAGACTAGAGTGTCT 362
Qy      123 HisPheGlySerThrAsnSerleuLeuTytrLeuAsnProArgLeuLyshisIleThGly 142
      363 CAGTTTGTCTTACTCAATGCGTCTCTACCTTGATCTTTCAAGCATATATACACA 422
Qy      143 TyrMetAlaProLeuValAspSerLeuGlnIlysluGlyTyrAlaAspGlyThrleu 162
      423 TACATGACACCATTTGGTGGAGTCTATATACACACTTGGCTACAAAGATACCGAATCTT 482
Db      163 PheGlyAlaProTytrAspPheArgTytrGlyLeuAlaGluGlyHisProSerGlnVal 182
      483 TTGGAGCTCCATATGATTTTCGTACGGGTACATCCGAGAGACATCTTGTGATGTC 542
Qy      183 GlySerlyspheleuLyAspLeuLyAsnLeuIleGluAlaSerAsnSer 200
      543 GCGTCAACTTACCTCCAAACCTAAAGCAGTTATCGAAAGCGAACACACACT 596

RESULT 12
Bg127829      724 bp      mRNA      linear      EST 31-JAN-2001
LOCUS      EST473475 tomato shoot/meristem Lycopersicon esculentum cDNA clone
DEFINITION      cDNA library 5' sequence, mRNA sequence.
ACCESSION      BG127829
VERSION      BG127829.1 GI:12628017

```

KEYWORDS	EST.
SOURCE	tomato.
ORGANISM	Lycopersicon esculentum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
	Lycopersicon.
REFERENCE	1 (bases 1 to 724)
AUTHORS	van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T., Hansen, C., Konning, C. and Tanksley, S.
TITLE	Generation of ESTs from tomato shoot/meristem tissue
JOURNAL	Unpublished (2001)
COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html . Location/Qualifiers
FEATURES	1..724
SOURCE	/organism="Lycopersicon esculentum" /cultivar="TA496" /db_xref="taxon:4081" /clone="CTOP18A6" /clone_lib="tomato shoot/meristem" /tissue_type="shoot/meristem" /dev_stage="developing shoots from 4-6wks old plants" /lab_host="SOLR" /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
BASE COUNT	238 a 138 c 124 g 224 t
ORIGIN	
Alignment Scores:	
Prod. No.:	1.15e-62 Length: 724
Score:	590.50 Matches: 126
Percent Similarity:	59.07% Conservative: 27
Best Local Similarity:	48.65% Mismatches: 45
Query Match:	25.31% Indels: 63
DB:	12 Gaps: 1
US-09-857-612A-14 (1-443) x BG127829 (1-724)	
QY	11 TlGcLuVAlAaThrLeuThrValThrValValValMetLeuSerLeuLeuGysThr 30 ::: :::: :::::
Db	131 TTACGCATGAAGAGCTCAATCATATTCATATATCAAAAGTGTGCACATATGCCAA 190
QY	31 CysGluValAsenSerLeuAspProLeuIleLeuIleProGlyAsnGlyLysnGlnLeu 50 ::: :::::
Db	191 GCAATTACTACTATCTCAACCCCTCAATCTTATATCCAGAGCTGGTGGAAACCAATTA 250
QY	51 GluAlaArgLeuThrAsnGlnGlyLysProSerThrPheIleCysGluSerTrpTrpPro 70 ::::: :::::
Db	251 GAGCAAGATTAATCTCAAGTACCAAGCCTACACAGCTTATTGGCAACAAGTTGATCCA 310
QY	71 LeuIleLysLysLysAsnGlyTrpPheArgLeuTrpPheAspSerSerValIleLeuAla 90
Db	311 TTAAATGAAGATAGTGAAAGAA----- 333
QY	91 ProPheTrpGlnCysPheAlaGluAlaGlyMetThrLeuHisTyrHisGlnGluLeuAspSP 110 ----- 333
Db	333 ----- 333
QY	111 TyrPheAsnThrProGlyValGluThrArgValProHisPheGlySerThrAsnSerLeu 130 ----- 333
Db	333 ----- 333
QY	131 LeuTyrLeuAsnProArgLeuLysHisIleThrGlyTyrMetAlaProLeuValAspSer 150
Db	334 -----ATTACAGCACTATATATGAGGCACTTGTGAAGACT 366
QY	151 LeuGlnLysLeuGlyTyrAlaAspGlyGluThrLeuPheGluValaProTyrAspPheArg 170

Db	367	TTTGAGAAATAGAGTATAGAGATGCTGCAATATCTGTTTGAGACACCTACAGATTTTTCGT	426
Oy	171	TyrGlyLeuAlaAlaGluGlyHisProSerGlnValGlySerLysPheLeuLysAspLeu	190
Db	427	TATGTTGGCTGGCGAGAGGTCATCAAGGTCAATGTCGTTGCGAATATCTCAGAGACTTG	486
Oy	191	LysAsnLeuIleGluValLeuSerAsnSerAsnGlyLysProValIleLeuLeuSer	210
Db	487	AAAGACATGATAGAAAGTGCAGATTAATTCAAATGGAGGTAAACCTGATATCTGTTGCT	546
Oy	211	HisSerLeuGlyGlyLeuPheValLeuGlnLeuLeuAsnAAsGlnProProSerTyrArg	230
Db	547	ACACGTTAGGTGGCTTATGTCACAGACTACTCGTTCGTAATCAAAATGCTGGAGT	605
Oy	231	LysLysPheIleLysHisPheIleAlaLeuSerAlaProTyrGlyGlyAlaIleAspLys	250
Db	606	CAAAAGTACATCAAAACACTTATACCATTTGGCTCCACATGGGAGGAGAAAGTATGCAA	665
Oy	251	MetTyrThrPheAlaSerGlyAsnThrLeuGlyValProLeuValAspProLeuLeu	269
Db	666	ATGTCACATTTGGCTTCTGTGTAACACACTTGTGTGCTTAAAGTAATCCGTTACTC	722
RESULT 13			
BSG526525			
LOCUS	616 bp	mRNA	linear
DEFINITION	60-13 Stevia field grown leaf cDNA	Stevia rebaudiana	cDNA 5', mRNA
SEQUENCE			
ACCESSION	BSG526525		
VERSION	BSG526525.1	GI:16950014	
KEYWORDS	EST.		
SOURCE	Stevia rebaudiana.		
ORGANISM	Stevia rebaudiana		
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Asteridae: easterids II; Asterales; Asteraceae; Asteroideae; Heliantheae; Stevia.		
AUTHORS	1 (bases 1 to 616)		
TITLE	Brandle, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.		
JOURNAL	Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in diterpene synthesis		
COMMENT	Unpublished (2001)		
	Contact: Jim Brandle		
	Genomics and Biotechnology		
	Agriculture and Agri-Food Canada - SCPPRC		
	1391 Sandford St., London, Ontario, CANADA, N5V 4T3		
	Tel: 519 457 1470		
	Fax: 519 457 3997		
	Email: jbrandle@eem.agr.ca		
	Seq primer: T3 promoter primer.		
	location/Qualifiers		
FEATURES			
source			
	1..616		
	/organism="Stevia rebaudiana"		
	/strain="751/1501"		
	/cultivar="Landrace"		
	/db_xref="taxon:55670"		
	/clone_lib="Stevia field grown leaf cDNA"		
	/tissue_type="leaf"		
	/dev_stage="field grown, mid-size"		
	/lab_host="E. coli strain XL0R"		
	/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from polyA+ enriched mRNA from field grown leaves. Mid-size actively growing leaves were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The cDNA was prepared using an xhoI-poly(dT) linker-primer. An EcoRI adapter was ligated to the blunt end cDNA and the products were digested with EcoRI and XhoI enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the host strain XL1-Blue MR". Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XL0R. Single pass DNA sequencing was performed using the T3		

promoter primer: 5' ATTAACCCCTACTAAGGGA 3'. This library was constructed by Alex Richman.

BASE COUNT 168 a 117 c 162 g 161 t 8 others

ORIGIN

Alignment Scores:

Pred. No.:	1.35e-60	Length:	616
Score:	573.00	Matches:	112
Percent Similarity:	80.24%	Conservative:	22
Best Local Similarity:	67.07%	Mismatches:	31
Query Match:	24.56%	Indels:	2
DB:	12	Gaps:	0

US-09-857-612A-14 (1-443) x BG526525 (1-616)

OY 224 ATGASPPROPSERTTPRARGLYSLYSPhelleLysHisPheleAlaLeuSerAlaPro 243
|||||
DB 3 CGTAAACCCACCCCTCATGGGCAACAAATACATTAAACATTTTATCCGNTGCCGACCA 62
OY 244 TTPGlyGlyAlaAlaLeuSpLumeTyrThrPheAlaSerGlyYasnThrLeuGly-ValPr 263
|||||
DB 63 TGGGTGGAGACGGTTGACAGATGTTACTTTGCTTGGGAACACTCTGGGAAGTTCC 122
OY 263 OLeuValAspProLeuLeuValArgAspGluGlnArgSerSerGluSerAsnLeuTrpLe 283
|||||
DB 123 ACTGTGAGAACCCGTTGCTGTCAGAAATGACCAACGAGTTCTGAAACCATTTATGGCC 182
OY 283 uLeuProAsnProLysLlePheGlyProGlnLysProLleValLleThrProLleArgPr 303
|||||
DB 183 CATGCCACGACGAAAAAATTTCCCTCAACAGACACTGTTCACATTCACATTCAC 242
OY 303 oTyrSerAlaHisAspMetValAspPheLeuLysAspLleGlyPheProGluGlnValTy 323
|||||
DB 243 TTAAGTGTCTTTTGGACATTTCACGGTTTCTTAAGATATCGGTTGCAAGAGGGTGCA 302
OY 323 rProTyrGluThrArgLleLeuProLeuLleGlyAsnLleLysAlaProGlnLysProLl 343
|||||
DB 303 CCTTACGAGACACGAATCTTGCTTGGTGAAGATTGGTTGATGGTGCACCGGAGTGCCTG 362
OY 343 eThrCysLleMetGlyThrGlyValGlyThrLeuGluThrLeuPheTyrGlyLysGlyAs 363
|||||
DB 363 AACGTCTAAGATGGAAAGCGGTGCCGACACCGGAACCTTGTATTAAGGACGACGACG 422
OY 363 pPheAspGluArgProGluLleSerTyrGlyAspGlyValAspGlyThrValAsnLeuVal-S 383
|||||
DB 423 GTTCGATTAAGCAGCCGGAATTTGTTATGAGATGTGTGACGAGCGTGATATGTGTGAG 482
OY 383 eXLeuAlaLeuGln 388
|||||
DB 483 GTTGTGTTGGCTTGGAG 499

RESULT 14 BE355801 537 bp mRNA linear EST 20-JUL-2000
BE353801

DEFINITION DGI_11.E05.b1_A002 Dark Grown 1 (DGI) Sorghum bicolor cDNA, mRNA
sequence.

ACCESSION BE355801
KEYWORDS BE355801.1 GI:9296903
SOURCE EST.

ORGANISM sorghum
Sorghum bicolor

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC

REFERENCE 1 (bases 1 to 537)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
,L.H.

TITLE An EST database from Sorghum: dark-grown seedlings
JOURNAL Unpublished (2000)

COMMENT Laboratory: Cordonnier-Pratt MM
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp@prattuga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below phred quality 16. The threshold for highest quality sequence
is 20.

Seq primer: JEN REV
High quality sequence stop: 460
POLYA-No.

FEATURES
source Location/Qualifiers
1..537
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGI)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision."

BASE COUNT 63 a 201 c 194 g 79 t

Alignment Scores:

Pred. No.:	3.37e-59	Length:	537
Score:	561.00	Matches:	104
Percent Similarity:	74.01%	Conservative:	27
Best Local Similarity:	58.76%	Mismatches:	44
Query Match:	24.05%	Indels:	2
DB:	10	Gaps:	2

US-09-857-612A-14 (1-443) x BE355801 (1-537)

OY 60 ProSerThrPheHleCysGluSerTPRTPRProLeuLleLysLysAsnGlyTrpPhe 79
|||||
DB 2 CCGTCCAGCCTCGTGTGCGCGGTGTG--CCACTGTGCGCGCCCGCGCGGTGTC 58

OY 80 ArgLeuTrpPheAspSerSerValLleLeuAlaProPheThrGlnCysPheAlaGluArg 99
|||||
DB 59 CGGCTGTGGTTCACACCCCTCGTGTGTGTGCGCGCGGTCAACAGGTGCTTGGCGACGG 118

OY 100 MetThrLeuHisTyrHisGlnGluLeuAspAspTyrPheAsnThrProGlyValGluThr 119
|||||
DB 119 ATGACGCTCTCCATACGACCGCGACCGGACGACTACCGGACCGCGCGGTGTGAGACC 178

OY 120 ArgValProHisPheGlySerThrAsnSerLeuLeuTyrLeuAsnProArgLeuLysHis 139
|||||
DB 179 AGGGTCTCCGACTTCGGCTCACCTCCACCTCGGCTACCTGACACCCCAACCTCAAGCTC 238

OY 140 IleThrGlyTyrMetAlaProLeuValAspSerLeu--GlnLysLeuGlyTyrAlaAsp 158
|||||
DB 239 CTGACGGGTACATGAACAACCTCTGGCGACGACCGCTGAGAGAGAGAGCGGCTACGAGGAG 298

OY 159 GlyGluThrLeuPheGlyAlaProTyrAspPheArgTyrGlyLeuAlaGluGlyHis 178
|||||
DB 299 GGGCGGACCTGTTGGCGCGCGGTACGACTTCGGTACGCGGTGCGCGCGCGGCGGCGAC 358

OY 179 ProSerGlnValGlySerLysPheLeuLysAspLeuLysAsnLeuLleGluGluAlaSer 198
|||||
DB 359 CCGTCCAGGTGGGACAGCGCTGACGAGCGCTGAGGTGAGGTGGGTGGCGCTGC 418

OY 199 AsnSerAsnGlnLysProValLleLeuLeuSerHisSerLeuGlnGlyLeuPheVal 218
|||||
DB 419 GCGGCGAAGCGGGGCGCGCGCGGATCTGTGTGGCGACAGCGCTGCGGCGGCTTGGCGG 478

OY 219 LeuGlnLeuLeuAsnArgAsnProProSerTPRArgLysLysPheLleLys 235
|||||
DB 479 CTCACAGCTGTGGCGGCGACCGCGCGCTGTGGCGGCGGCGACGATGCGAG 529

RESULT 15 B0864610 527 bp mRNA linear EST 14-AUG-2002
B0864610

DEFINITION OGC27C22.y9.ab1 OG_ABCDI lettuce salinas lactuca sativa cDNA clone
OGC27C22, mRNA sequence.
ACCESSION B0864610

